

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 26, 2004, 15:30:32 ; Search time 50.5 Seconds
(without alignments)
44.760 Million cell updates/sec

Title: US-09-668-314C-71
Perfect score: 8
Sequence: 1 EVNLDAEF 8

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1586107 seqs, 282547505 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%	Query					Description
No.	Score	Match	Length	DB	ID			
1	8	100.0	8	3	AAY94771			Aay94771 Beta-secr
2	8	100.0	8	4	AAE10661			Aae10661 Human asp
3	8	100.0	8	4	AAE02613			Aae02613 Human Asp
4	8	100.0	8	5	ABB78622			Abb78622 Human bet
5	8	100.0	8	6	ABR54159			Abr54159 Beta-secr
6	8	100.0	9	2	AAW82081			Aaw82081 Fluorogen
7	8	100.0	9	3	AAB07874			Aab07874 A peptide
8	8	100.0	9	3	AAB07894			Aab07894 Substrate
9	8	100.0	9	4	AAG73297			Aag73297 Protease

10	8	100.0	9	5	ABB06519	Abb06519	Beta-secr
11	8	100.0	9	5	ABB09003	Abb09003	Peptide #
12	8	100.0	9	5	ABU60429	Abu60429	Protease
13	8	100.0	9	5	ABU60441	Abu60441	Protease
14	8	100.0	9	5	AAE16663	Aae16663	Oligopept
15	8	100.0	9	5	AAU74837	Aau74837	Synthetic
16	8	100.0	9	5	ABB07598	Abb07598	Synthetic
17	8	100.0	9	5	AAM50897	Aam50897	Oligopept
18	8	100.0	9	6	ABP97975	Abp97975	Synthetic
19	8	100.0	9	6	ABP57515	Abp57515	Different
20	8	100.0	9	6	ABP57084	Abp57084	Synthetic
21	8	100.0	9	6	ABP71468	Abp71468	Beta-secr
22	8	100.0	9	6	AAO16449	Aao16449	Beta-secr
23	8	100.0	9	6	ABP71269	Abp71269	Oligopept
24	8	100.0	9	6	ABR44377	Abr44377	Oligonpep
25	8	100.0	9	6	ABP58375	Abp58375	Beta-secr
26	8	100.0	9	6	AAO26801	Aao26801	Beta-secr
27	8	100.0	9	6	ABG75940	Abg75940	Synthetic
28	8	100.0	9	6	ABP71630	Abp71630	Beta-secr
29	8	100.0	9	6	AAE36000	Aae36000	APP subst
30	8	100.0	9	6	ABR82372	Abr82372	Beta-secr
31	8	100.0	9	6	ABR56258	Abr56258	Amyloid P
32	8	100.0	9	6	ABR62018	Abr62018	Beta-secr
33	8	100.0	9	6	ABR61887	Abr61887	Beta-secr
34	8	100.0	9	7	ABR56195	Abr56195	Amyloid p
35	8	100.0	9	7	ADC29723	Adc29723	Synthetic
36	8	100.0	9	7	ADC26557	Adc26557	Beta-secr
37	8	100.0	9	7	ADC10532	Adc10532	Synthetic
38	8	100.0	9	7	ADD80769	Add80769	Synthetic
39	8	100.0	10	2	AAW08362	Aaw08362	Beta-secr
40	8	100.0	10	2	AAZ33756	Aaz33756	Synthetic
41	8	100.0	10	3	AAZ69707	Aaz69707	Beta-APP
42	8	100.0	10	4	AAU07226	Aau07226	Human bet
43	8	100.0	10	4	AAE10653	Aae10653	Human APP
44	8	100.0	10	4	AAE06898	Aae06898	Human amy
45	8	100.0	10	4	AAB61337	Aab61337	Swedish m
46	8	100.0	10	4	AAE02605	Aae02605	Human APP
47	8	100.0	10	4	AAB66575	Aab66575	Synthetic
48	8	100.0	10	4	AAB47266	Aab47266	Peptide 5
49	8	100.0	10	4	AAU06627	Aau06627	Synthetic
50	8	100.0	10	5	ABB06425	Abb06425	Human APP
51	8	100.0	10	5	ABG78376	Abg78376	Human bet
52	8	100.0	10	5	ABB78614	Abb78614	Beta-secr
53	8	100.0	10	5	AAU99491	Aau99491	Peptide #
54	8	100.0	10	5	ABG30941	Abg30941	Nogo/BACE
55	8	100.0	10	6	ABP57509	Abp57509	Different
56	8	100.0	10	6	ABG76104	Abg76104	Amyloid p
57	8	100.0	10	6	ABR61932	Abr61932	Human amy
58	8	100.0	10	6	ABR62009	Abr62009	Substrate
59	8	100.0	10	6	ADA74820	Ada74820	Human amy
60	8	100.0	10	7	ABR84672	Abr84672	Aggrecona
61	8	100.0	11	4	AAB97469	Aab97469	Asp2 subs
62	8	100.0	11	4	AAB75145	Aab75145	Asp 1 sub
63	8	100.0	11	4	AAB75142	Aab75142	APP Swedi
64	8	100.0	12	5	ABG78396	Abg78396	Memapsin
65	8	100.0	12	5	ABB08996	Abb08996	Amyloid p
66	8	100.0	12	5	AAE16656	Aae16656	APP subst

67	8	100.0	12	5	AAU74830	Aau74830	Synthetic
68	8	100.0	12	5	ABB07591	Abb07591	Biotinylna
69	8	100.0	12	6	ABP97968	Abp97968	A synthet
70	8	100.0	12	6	AAO26794	Aao26794	Beta-secr
71	8	100.0	12	7	ADC29716	Adc29716	Synthetic
72	8	100.0	12	7	ADD80762	Add80762	Synthetic
73	8	100.0	13	5	ABB06591	Abb06591	Beta-secr
74	8	100.0	13	5	AAM50890	Aam50890	Fluoresce
75	8	100.0	13	6	ABP57077	Abp57077	Synthetic
76	8	100.0	13	6	ABP71461	Abp71461	Beta-secr
77	8	100.0	13	6	AAO16442	Aao16442	Beta-secr
78	8	100.0	13	6	ABP71262	Abp71262	Synthetic
79	8	100.0	13	6	ABR44370	Abr44370	Synthetic
80	8	100.0	13	6	ABP58368	Abp58368	Synthetic
81	8	100.0	13	6	ABG75933	Abg75933	Synthetic
82	8	100.0	13	6	ABP71623	Abp71623	Beta-secr
83	8	100.0	13	6	AAE35993	Aae35993	APP subst
84	8	100.0	13	6	ABR42268	Abr42268	Amyloid p
85	8	100.0	13	6	ABR82365	Abr82365	Synthetic
86	8	100.0	13	6	ABR56251	Abr56251	Amyloid P
87	8	100.0	13	6	ABR62011	Abr62011	Amino aci
88	8	100.0	13	6	ABR61880	Abr61880	Beta-secr
89	8	100.0	13	7	ABR56172	Abr56172	Amyloid p
90	8	100.0	13	7	ADC10524	Adc10524	Synthetic
91	8	100.0	13	7	ADC81567	Adc81567	P33K-BACE
92	8	100.0	16	3	AAB06316	Aab06316	Human bet
93	8	100.0	18	4	AAE00609	Aae00609	Beta-amyl
94	8	100.0	19	4	AAE00611	Aae00611	Amyloid p
95	8	100.0	20	2	AAW82211	Aaw82211	Fluorogen
96	8	100.0	20	3	AAV69714	Aay69714	Beta-APP
97	8	100.0	20	4	AAG73229	Aag73229	Protease
98	8	100.0	20	5	AAU78509	Aau78509	Beta amyl
99	8	100.0	21	2	AAW08361	Aaw08361	Beta-secr
100	8	100.0	21	2	AAW82186	Aaw82186	Fluorogen
101	8	100.0	21	2	AAV33755	Aay33755	Synthetic
102	8	100.0	21	4	AAG73204	Aag73204	Protease
103	8	100.0	21	4	AAG73203	Aag73203	Protease
104	8	100.0	21	4	AAB47265	Aab47265	Peptide 5
105	8	100.0	23	4	AAB97474	Aab97474	Asp2 subs
106	8	100.0	23	4	AAB75148	Aab75148	Asp 1 sub
107	8	100.0	23	7	ADC81568	Adc81568	P33K-BACE
108	8	100.0	30	2	AAW08360	Aaw08360	Beta-secr
109	8	100.0	30	2	AAV33754	Aay33754	Synthetic
110	8	100.0	30	3	AAB07895	Aab07895	Substrate
111	8	100.0	30	4	AAB47264	Aab47264	Peptide 2
112	8	100.0	30	5	ABB09004	Abb09004	Peptide #
113	8	100.0	30	5	AAE16664	Aae16664	Oligopept
114	8	100.0	30	5	AAU74838	Aau74838	Synthetic
115	8	100.0	30	5	ABB07599	Abb07599	Synthetic
116	8	100.0	30	5	AAM50898	Aam50898	Oligopept
117	8	100.0	30	6	ABP97976	Abp97976	Synthetic
118	8	100.0	30	6	ABP57085	Abp57085	Synthetic
119	8	100.0	30	6	ABP71469	Abp71469	Beta-secr
120	8	100.0	30	6	AAO16450	Aao16450	Beta-secr
121	8	100.0	30	6	ABP71270	Abp71270	Oligopept
122	8	100.0	30	6	ABR44378	Abr44378	Oligonpep
123	8	100.0	30	6	ABP58376	Abp58376	Beta-secr

124	8	100.0	30	6	AAO26802	Aao26802	Beta-secr
125	8	100.0	30	6	ABG75941	Abg75941	Synthetic
126	8	100.0	30	6	ABP71631	Abp71631	Beta-secr
127	8	100.0	30	6	AAE36001	Aae36001	APP subst
128	8	100.0	30	6	ABR82373	Abr82373	Beta-secr
129	8	100.0	30	6	ABR56259	Abr56259	Amyloid P
130	8	100.0	30	6	ABR62019	Abr62019	Beta-secr
131	8	100.0	30	6	ABR61888	Abr61888	Beta-secr
132	8	100.0	30	7	ABR56196	Abr56196	Amyloid p
133	8	100.0	30	7	ADC29724	Adc29724	Synthetic
134	8	100.0	30	7	ADC10531	Adc10531	Synthetic
135	8	100.0	30	7	ADD80770	Add80770	Synthetic
136	8	100.0	32	2	AAW04402	Aaw04402	Mouse amy
137	8	100.0	32	2	AAW04403	Aaw04403	Mouse amy
138	8	100.0	32	2	AAW04401	Aaw04401	Mouse amy
139	8	100.0	32	5	ABB08999	Abb08999	Amyloid p
140	8	100.0	32	5	AAE16659	Aae16659	APP subst
141	8	100.0	32	5	AAU74833	Aau74833	Synthetic
142	8	100.0	32	5	ABB07594	Abb07594	Biotinyla
143	8	100.0	32	6	ABP97971	Abp97971	A synthet
144	8	100.0	32	6	AAO26797	Aao26797	Beta-secr
145	8	100.0	32	7	ADC29719	Adc29719	Synthetic
146	8	100.0	32	7	ADD80765	Add80765	Synthetic
147	8	100.0	33	2	AAW08359	Aaw08359	Beta-secr
148	8	100.0	33	2	AAV33753	Aay33753	Synthetic
149	8	100.0	33	3	AAB07892	Aab07892	Substrate
150	8	100.0	33	4	AAB47263	Aab47263	Peptide 1
151	8	100.0	33	5	ABB09001	Abb09001	P26-P4'SW
152	8	100.0	33	5	AAE16661	Aae16661	P26-P4'SW
153	8	100.0	33	5	AAU74835	Aau74835	Synthetic
154	8	100.0	33	5	ABB07596	Abb07596	Biotinyla
155	8	100.0	33	5	AAM50893	Aam50893	Fluoresce
156	8	100.0	33	5	AAM50895	Aam50895	P26-P4'SW
157	8	100.0	33	6	ABP97973	Abp97973	Synthetic
158	8	100.0	33	6	ABP57082	Abp57082	P26-P4'SW
159	8	100.0	33	6	ABP71466	Abp71466	Beta-secr
160	8	100.0	33	6	AAO16445	Aao16445	Beta-secr
161	8	100.0	33	6	AAO16447	Aao16447	Beta-secr
162	8	100.0	33	6	ABP71267	Abp71267	Synthetic
163	8	100.0	33	6	ABR44375	Abr44375	P26-P4' S
164	8	100.0	33	6	ABP58373	Abp58373	Beta-secr
165	8	100.0	33	6	AAO26799	Aao26799	Beta-secr
166	8	100.0	33	6	ABG75938	Abg75938	Beta-secr
167	8	100.0	33	6	ABP71628	Abp71628	Beta-secr
168	8	100.0	33	6	AAE35998	Aae35998	P26-P4'SW
169	8	100.0	33	6	ABR42273	Abr42273	Amyloid p
170	8	100.0	33	6	ABR42271	Abr42271	Amyloid p
171	8	100.0	33	6	ABR82370	Abr82370	Beta-secr
172	8	100.0	33	6	ABR56256	Abr56256	Amyloid P
173	8	100.0	33	6	ABR56254	Abr56254	Amyloid P
174	8	100.0	33	6	ABR62016	Abr62016	Beta-secr
175	8	100.0	33	6	ABR62014	Abr62014	Amino aci
176	8	100.0	33	6	ABR61885	Abr61885	Beta-secr
177	8	100.0	33	6	ABR61883	Abr61883	Beta-secr
178	8	100.0	33	7	ABR56177	Abr56177	Amyloid p
179	8	100.0	33	7	ABR56175	Abr56175	Amyloid p
180	8	100.0	33	7	ADC29721	Adc29721	Synthetic

181	8	100.0	33	7	ADC10529	Adc10529	Synthetic
182	8	100.0	33	7	ADD80767	Add80767	Synthetic
183	8	100.0	34	6	ABP57080	Abp57080	Synthetic
184	8	100.0	34	6	ABP71464	Abp71464	Beta-secr
185	8	100.0	34	6	ABP71265	Abp71265	Synthetic
186	8	100.0	34	6	ABR44373	Abr44373	Synthetic
187	8	100.0	34	6	ABP58371	Abp58371	Synthetic
188	8	100.0	34	6	ABG75936	Abg75936	Synthetic
189	8	100.0	34	6	ABP71626	Abp71626	Beta-secr
190	8	100.0	34	6	AAE35996	Aae35996	APP subst
191	8	100.0	34	6	ABR82368	Abr82368	Synthetic
192	8	100.0	34	7	ADC10527	Adc10527	Synthetic
193	8	100.0	39	3	AAY69718	Aay69718	Beta-APP
194	8	100.0	42	2	AAW08350	Aaw08350	Wild type
195	8	100.0	42	2	AAY33752	Aay33752	Synthetic
196	8	100.0	42	4	AAB47262	Aab47262	Peptide 2
197	8	100.0	58	2	AAW98001	Aaw98001	Swedish-F
198	8	100.0	63	7	ADB33538	Adb33538	APP regio
199	8	100.0	103	2	AAR74698	Aar74698	Beta-amy1
200	8	100.0	115	2	AAW98000	Aaw98000	SwedishLo
201	8	100.0	115	2	AAW97997	Aaw97997	Swedish-F
202	8	100.0	261	4	AAE00610	Aae00610	Chimeric
203	8	100.0	506	2	AAW61152	Aaw61152	Maltose b
204	8	100.0	506	2	AAY33742	Aay33742	MBP-APP (
205	8	100.0	506	4	AAB47258	Aab47258	MBP:APP C
206	8	100.0	695	3	AAY88435	Aay88435	Human APP
207	8	100.0	695	4	AAU07206	Aau07206	Human bet
208	8	100.0	695	4	AAE10633	Aae10633	Human amy
209	8	100.0	695	4	AAE06863	Aae06863	Human amy
210	8	100.0	695	4	AAE02585	Aae02585	Human amy
211	8	100.0	695	4	AAU06607	Aau06607	Human Amy
212	8	100.0	695	5	ABB78594	Abb78594	Human APP
213	8	100.0	695	7	ADB87313	Adb87313	Human amy
214	8	100.0	697	3	AAY88429	Aay88429	Human APP
215	8	100.0	697	4	AAU07209	Aau07209	Human bet
216	8	100.0	697	4	AAE10636	Aae10636	Human amy
217	8	100.0	697	4	AAE06866	Aae06866	Human amy
218	8	100.0	697	4	AAE02588	Aae02588	Human amy
219	8	100.0	697	4	AAU06610	Aau06610	Human Amy
220	8	100.0	697	5	ABB78597	Abb78597	Human APP
221	8	100.0	770	4	AAE06912	Aae06912	Human amy
222	8	100.0	783	7	ADB33503	Adb33503	Human APP
223	8	100.0	783	7	ADB33511	Adb33511	Human APP
224	8	100.0	941	7	ADB33507	Adb33507	Human APP
225	8	100.0	941	7	ADB33515	Adb33515	Human APP
226	7	87.5	11	5	AAM52699	Aam52699	Beta-secr
227	6	75.0	6	5	AAU78500	Aau78500	Beta secr
228	6	75.0	70	4	AAE09374	Aae09374	Human APP
229	6	75.0	278	3	AAB32698	Aab32698	Eucalyptu
230	6	75.0	326	6	ABU38743	Abu38743	Protein e
231	6	75.0	822	4	ABB57937	Abb57937	Drosophil
232	6	75.0	868	6	ABU49365	Abu49365	Protein e
233	6	75.0	4623	4	ABB71106	Abb71106	Drosophil
234	6	75.0	16368	6	ABM67171	Abm67171	Photorhab
235	5	62.5	5	2	AAW08217	Aaw08217	Swedish d
236	5	62.5	5	2	AAW61151	Aaw61151	APP Swedi
237	5	62.5	5	2	AAY33751	Aay33751	Swedish m

238	5	62.5	5	4	AAB47261	Aab47261	Swedish m
239	5	62.5	6	6	ABP57524	Abp57524	Peptide #
240	5	62.5	7	2	AAR72758	Aar72758	Antimalar
241	5	62.5	7	2	AAR72776	Aar72776	Mammalian
242	5	62.5	7	2	AAR72756	Aar72756	Antimalar
243	5	62.5	7	3	AAy83859	Aay83859	Ribonucle
244	5	62.5	9	2	AAW82085	Aaw82085	Fluorogen
245	5	62.5	9	2	AAW82082	Aaw82082	Fluorogen
246	5	62.5	9	3	AAB07875	Aab07875	A peptide
247	5	62.5	9	4	AAG73293	Aag73293	Protease
248	5	62.5	9	4	AAG73280	Aag73280	Protease
249	5	62.5	9	4	AAG73279	Aag73279	Protease
250	5	62.5	9	5	ABU60428	Abu60428	Protease
251	5	62.5	9	5	ABU60432	Abu60432	Protease
252	5	62.5	10	3	AAy69706	Aay69706	Beta-APP
253	5	62.5	10	3	AAy69705	Aay69705	Beta-APP
254	5	62.5	16	5	ABU60427	Abu60427	Protease
255	5	62.5	19	2	AAR55260	Aar55260	N-termina
256	5	62.5	20	3	AAy69715	Aay69715	Beta-APP
257	5	62.5	20	4	AAG73201	Aag73201	Protease
258	5	62.5	20	4	AAG73333	Aag73333	Protease
259	5	62.5	20	4	AAG73202	Aag73202	Protease
260	5	62.5	20	4	AAG73315	Aag73315	Protease
261	5	62.5	21	2	AAW82187	Aaw82187	Fluorogen
262	5	62.5	21	2	AAW82190	Aaw82190	Fluorogen
263	5	62.5	21	4	AAG73205	Aag73205	Protease
264	5	62.5	21	4	AAG73316	Aag73316	Protease
265	5	62.5	21	4	AAG73208	Aag73208	Protease
266	5	62.5	26	4	AAG73200	Aag73200	Protease
267	5	62.5	31	4	ABB40171	Abb40171	Peptide #
268	5	62.5	31	4	AAM33820	Aam33820	Peptide #
269	5	62.5	31	4	AAM73625	Aam73625	Human bon
270	5	62.5	31	4	ABG55358	Abg55358	Human liv
271	5	62.5	31	5	ABG43495	Abg43495	Human pep
272	5	62.5	51	5	ABP66668	Abp66668	Human bre
273	5	62.5	58	2	AAR32204	Aar32204	Apple fru
274	5	62.5	58	4	ABG02896	Abg02896	Novel hum
275	5	62.5	60	5	ABP31773	Abp31773	Human ORF
276	5	62.5	63	4	AAM18749	Aam18749	Peptide #
277	5	62.5	63	4	ABB37849	Abb37849	Peptide #
278	5	62.5	63	4	AAM31252	Aam31252	Peptide #
279	5	62.5	63	4	ABB23108	Abb23108	Protein #
280	5	62.5	63	4	AAM70969	Aam70969	Human bon
281	5	62.5	63	4	AAM58474	Aam58474	Human bra
282	5	62.5	63	4	ABG52690	Abg52690	Human liv
283	5	62.5	63	5	ABG40767	Abg40767	Human pep
284	5	62.5	65	5	ABP09510	Abp09510	Human ORF
285	5	62.5	67	2	AAW10169	Aaw10169	Rat brain
286	5	62.5	68	2	AAR32203	Aar32203	Apple fru
287	5	62.5	68	2	AAW10173	Aaw10173	Rat brain
288	5	62.5	70	4	AAU62064	Aau62064	Propionib
289	5	62.5	70	6	ABM58583	Abm58583	Propionib
290	5	62.5	71	6	ABU42889	Abu42889	Protein e
291	5	62.5	73	5	ABP06194	Abp06194	Human ORF
292	5	62.5	73	5	ABP39660	Abp39660	Staphyloc
293	5	62.5	81	5	AAU10747	Aau10747	Amino aci
294	5	62.5	91	3	AAG02458	Aag02458	Human sec

295	5	62.5	93	7	ADC32781	Adc32781	Human nov
296	5	62.5	97	4	ABG25706	Abg25706	Novel hum
297	5	62.5	100	3	AAy51923	Aay51923	Transgeni
298	5	62.5	104	4	AAE12897	Aae12897	Human rec
299	5	62.5	109	4	AAG90316	Aag90316	C glutami
300	5	62.5	110	5	ABP10932	Abp10932	Human ORF
301	5	62.5	110	6	ABP60082	Abp60082	Mouse RGS
302	5	62.5	111	6	ABP60083	Abp60083	Human RGS
303	5	62.5	115	4	AAU65327	Aau65327	Propionib
304	5	62.5	115	6	ABM61846	Abm61846	Propionib
305	5	62.5	116	2	AAy41022	Aay41022	RGS4 prot
306	5	62.5	116	2	AAy41021	Aay41021	RGS3 prot
307	5	62.5	116	3	AAy87823	Aay87823	Human APP
308	5	62.5	117	3	AAy51925	Aay51925	Transgeni
309	5	62.5	117	4	AAU54216	Aau54216	Propionib
310	5	62.5	117	4	AAE12896	Aae12896	Human rec
311	5	62.5	117	6	ABM50735	Abm50735	Propionib
312	5	62.5	118	2	AAy41000	Aay41000	Rat RGS4
313	5	62.5	119	4	AAO11644	Aao11644	Human pol
314	5	62.5	126	5	ABB47408	Abb47408	Listeria
315	5	62.5	128	7	ABR82620	Abr82620	Rat RGS4
316	5	62.5	132	5	ABB06009	Abb06009	Human can
317	5	62.5	132	6	ABP97162	Abp97162	Human epo
318	5	62.5	133	6	ABM65768	Abm65768	Propionib
319	5	62.5	134	4	AAB63564	Aab63564	Human gas
320	5	62.5	136	2	AAW89028	Aaw89028	Polypepti
321	5	62.5	136	4	ABB51128	Abb51128	Human sec
322	5	62.5	136	6	ABO45385	Abo45385	Novel hum
323	5	62.5	136	7	ABO26865	Abo26865	Protein a
324	5	62.5	143	4	AAB95281	Aab95281	Human pro
325	5	62.5	145	4	AAU50508	Aau50508	Propionib
326	5	62.5	145	6	ABM47027	Abm47027	Propionib
327	5	62.5	146	4	AAM39726	Aam39726	Human pol
328	5	62.5	148	5	ABB47497	Abb47497	Listeria
329	5	62.5	148	6	ABU32673	Abu32673	Protein e
330	5	62.5	151	6	ABU49793	Abu49793	Protein e
331	5	62.5	156	5	ABB06808	Abb06808	Human nGP
332	5	62.5	166	5	ABU05971	Abu05971	M. tuberc
333	5	62.5	167	5	AAU11043	Aau11043	Rat RGS4
334	5	62.5	169	6	ADA34292	Ada34292	Acinetoba
335	5	62.5	172	5	ABP11424	Abp11424	Human ORF
336	5	62.5	183	4	AAG91737	Aag91737	C glutami
337	5	62.5	184	4	AAM41512	Aam41512	Human pol
338	5	62.5	184	4	AAB50322	Aab50322	Human cyt
339	5	62.5	184	4	AAB94798	Aab94798	Human pro
340	5	62.5	184	5	AAU91298	Aau91298	Human pro
341	5	62.5	184	5	ABP51778	Abp51778	Human mac
342	5	62.5	193	5	ABP29248	Abp29248	Streptoco
343	5	62.5	197	2	AAW10221	Aaw10221	Haemophil
344	5	62.5	197	6	ABR53722	Abr53722	Protein s
345	5	62.5	205	3	AAB25173	Aab25173	Eucalyptu
346	5	62.5	205	5	AAU78976	Aau78976	Human RGS
347	5	62.5	205	7	ADE62388	Ade62388	Human Pro
348	5	62.5	205	7	ADE62386	Ade62386	Rat Prote
349	5	62.5	205	7	ADE62390	Ade62390	Rat Prote
350	5	62.5	205	7	ADE62392	Ade62392	Human Pro
351	5	62.5	206	6	ABM69365	Abm69365	Phototrab

352	5	62.5	207	2	AAW20276	Aaw20276	H. pylori
353	5	62.5	208	2	AAW20824	Aaw20824	H. pylori
354	5	62.5	217	2	AAR34723	Aar34723	E. coli B
355	5	62.5	217	2	AAR73968	Aar73968	Nitroredu
356	5	62.5	217	2	AAR76580	Aar76580	E. coli n
357	5	62.5	217	2	AAR95880	Aar95880	Bacterium
358	5	62.5	217	2	AAW13084	Aawl3084	Escherich
359	5	62.5	217	2	AAW13083	Aawl3083	Escherich
360	5	62.5	217	4	AAU29347	Aau29347	Novel mar
361	5	62.5	217	6	ABP70756	Abp70756	Mutant E.
362	5	62.5	217	6	ABP70759	Abp70759	Mutant E.
363	5	62.5	217	6	ABP70754	Abp70754	Mutant E.
364	5	62.5	217	6	ABP70738	Abp70738	Wild-type
365	5	62.5	217	6	ABP70757	Abp70757	Mutant E.
366	5	62.5	217	6	ABP70753	Abp70753	Mutant E.
367	5	62.5	217	6	ABP70755	Abp70755	Mutant E.
368	5	62.5	217	6	ABP70758	Abp70758	Mutant E.
369	5	62.5	217	6	ABP70750	Abp70750	Mutant E.
370	5	62.5	217	6	ABP70752	Abp70752	Mutant E.
371	5	62.5	217	6	ABP70751	Abp70751	Mutant E.
372	5	62.5	220	5	AAE19856	Aae19856	Mouse TRI
373	5	62.5	227	5	ABP64054	Abp64054	Human ORF
374	5	62.5	235	3	AAY97153	Aay97153	Human reg
375	5	62.5	235	3	AAG29884	Aag29884	Arabidops
376	5	62.5	235	5	AAE25829	Aae25829	Human reg
377	5	62.5	235	5	AAU10749	Aau10749	Human RGS
378	5	62.5	235	5	ABP64801	Abp64801	Human pro
379	5	62.5	255	2	AAY31833	Aay31833	Human foe
380	5	62.5	255	4	AAB73684	Aab73684	Human oxi
381	5	62.5	255	4	AAU29292	Aau29292	Human PRO
382	5	62.5	255	4	ABG02357	Abg02357	Novel hum
383	5	62.5	255	5	AAU96195	Aau96195	Human sec
384	5	62.5	255	5	AAU96170	Aau96170	Human sec
385	5	62.5	255	5	ABG64818	Abg64818	Human alb
386	5	62.5	255	5	ABG64819	Abg64819	Human alb
387	5	62.5	255	6	ABU58668	Abu58668	Human PRO
388	5	62.5	255	6	ABU88216	Abu88216	Novel hum
389	5	62.5	255	6	ABU84531	Abu84531	Human sec
390	5	62.5	255	6	ABR66405	Abr66405	Human sec
391	5	62.5	255	6	ABR65795	Abr65795	Human sec
392	5	62.5	255	6	ABU99735	Abu99735	Human sec
393	5	62.5	255	6	ABU82974	Abu82974	Human PRO
394	5	62.5	255	6	ABU90095	Abu90095	Novel hum
395	5	62.5	255	6	ABR68344	Abr68344	Human sec
396	5	62.5	255	6	ABU96397	Abu96397	Novel hum
397	5	62.5	255	6	ABU92828	Abu92828	Human sec
398	5	62.5	255	6	ABO08905	Abo08905	Human sec
399	5	62.5	255	6	ABO02957	Abo02957	Human sec
400	5	62.5	255	6	ABR75111	Abr75111	Human sec
401	5	62.5	255	6	ABR94873	Abr94873	Human sec
402	5	62.5	255	6	ABU85846	Abu85846	Human PRO
403	5	62.5	255	6	ABU99006	Abu99006	Novel hum
404	5	62.5	255	6	ABU98221	Abu98221	Novel hum
405	5	62.5	255	6	ABU91927	Abu91927	Novel hum
406	5	62.5	255	6	ABU89620	Abu89620	Human PRO
407	5	62.5	255	6	ABU86461	Abu86461	Human sec
408	5	62.5	255	6	ABU67674	Abu67674	Human sec

409	5	62.5	255	6	ABU80702	Abu80702	Human	PRO
410	5	62.5	255	6	ABR99620	Abr99620	Human	sec
411	5	62.5	255	6	ABR99010	Abr99010	Human	sec
412	5	62.5	255	6	ABO16533	Abo16533	Human	sec
413	5	62.5	255	6	ABR92433	Abr92433	Human	sec
414	5	62.5	255	6	ABO19074	Abo19074	Human	sec
415	5	62.5	255	6	ABR78495	Abr78495	Human	sec
416	5	62.5	255	6	ABU85231	Abu85231	Novel	hum
417	5	62.5	255	6	ABO00370	Abo00370	Novel	hum
418	5	62.5	255	6	ABO11702	Abo11702	Human	sec
419	5	62.5	255	6	ABO02347	Abo02347	Human	sec
420	5	62.5	255	6	ABU88921	Abu88921	Novel	hum
421	5	62.5	255	6	ABU83616	Abu83616	Human	sec
422	5	62.5	255	6	ABO06417	Abo06417	Novel	hum
423	5	62.5	255	6	ABR59453	Abr59453	Human	sec
424	5	62.5	255	6	ABO09515	Abo09515	Human	sec
425	5	62.5	255	6	ABO19379	Abo19379	Novel	hum
426	5	62.5	255	6	ABO11397	Abo11397	Human	sec
427	5	62.5	255	6	ABR67015	Abr67015	Human	sec
428	5	62.5	255	6	ABO16228	Abo16228	Human	sec
429	5	62.5	255	6	ABO13934	Abo13934	Human	sec
430	5	62.5	255	6	ABU65837	Abu65837	Human	sec
431	5	62.5	255	6	ABO07685	Abo07685	Human	PRO
432	5	62.5	255	6	ABO03872	Abo03872	Human	sec
433	5	62.5	255	6	ABR67320	Abr67320	Human	sec
434	5	62.5	255	6	ABO15923	Abo15923	Human	sec
435	5	62.5	255	6	ABU56204	Abu56204	Human	sec
436	5	62.5	255	6	ABU65532	Abu65532	Human	PRO
437	5	62.5	255	6	ABU95477	Abu95477	Novel	hum
438	5	62.5	255	6	ABU71380	Abu71380	Human	PRO
439	5	62.5	255	6	ABO07990	Abo07990	Human	PRO
440	5	62.5	255	6	ABR70231	Abr70231	Human	sec
441	5	62.5	255	6	ABR69564	Abr69564	Human	sec
442	5	62.5	255	6	ABO01705	Abo01705	Human	PRO
443	5	62.5	255	6	ABU81507	Abu81507	Human	PRO
444	5	62.5	255	6	ABR60304	Abr60304	Human	sec
445	5	62.5	255	6	ABR68039	Abr68039	Human	sec
446	5	62.5	255	6	ABR65427	Abr65427	Human	sec
447	5	62.5	255	6	ABR68649	Abr68649	Human	sec
448	5	62.5	255	6	ABR72061	Abr72061	Human	sec
449	5	62.5	255	6	ABU85541	Abu85541	Human	PRO
450	5	62.5	255	6	ABU89231	Abu89231	Human	sec
451	5	62.5	255	6	ABU83311	Abu83311	Human	sec
452	5	62.5	255	6	ABU95167	Abu95167	Novel	hum
453	5	62.5	255	6	ABU90715	Abu90715	Novel	hum
454	5	62.5	255	6	ABU84226	Abu84226	Human	sec
455	5	62.5	255	6	ABU93877	Abu93877	Novel	hum
456	5	62.5	255	6	ABR65122	Abr65122	Human	sec
457	5	62.5	255	6	ABR68954	Abr68954	Human	sec
458	5	62.5	255	6	ABO06770	Abo06770	Human	sec
459	5	62.5	255	6	ABR99315	Abr99315	Human	sec
460	5	62.5	255	6	ABU57199	Abu57199	Human	PRO
461	5	62.5	255	6	ABU86151	Abu86151	Novel	hum
462	5	62.5	255	6	ABU82438	Abu82438	Novel	hum
463	5	62.5	255	6	ABU87449	Abu87449	Human	PRO
464	5	62.5	255	6	ABU83921	Abu83921	Human	sec
465	5	62.5	255	6	ABO08295	Abo08295	Human	PRO

466	5	62.5	255	6	ABU82006	Abu82006	Novel	hum
467	5	62.5	255	6	ABU66170	Abu66170	Novel	hum
468	5	62.5	255	6	ABR59999	Abr59999	Human	sec
469	5	62.5	255	6	ABU94187	Abu94187	Novel	hum
470	5	62.5	255	6	ABO00060	Abo00060	Novel	hum
471	5	62.5	255	6	ABR66710	Abr66710	Human	sec
472	5	62.5	255	6	ABR91128	Abr91128	Human	sec
473	5	62.5	255	6	ABU94555	Abu94555	Human	PRO
474	5	62.5	255	6	ABU79437	Abu79437	Human	PRO
475	5	62.5	255	6	ABU86766	Abu86766	Human	sec
476	5	62.5	255	6	ABU87071	Abu87071	Novel	hum
477	5	62.5	255	6	ABU94860	Abu94860	Human	PRO
478	5	62.5	255	6	ABO04787	Abo04787	Human	PRO
479	5	62.5	255	6	ABR70536	Abr70536	Human	sec
480	5	62.5	255	6	ABU98701	Abu98701	Human	PRO
481	5	62.5	255	6	ABR66100	Abr66100	Human	sec
482	5	62.5	255	6	ABR64817	Abr64817	Human	sec
483	5	62.5	255	6	ABU79742	Abu79742	Human	PRO
484	5	62.5	255	6	ABU93133	Abu93133	Human	sec
485	5	62.5	255	6	ABU96092	Abu96092	Human	PRO
486	5	62.5	255	6	ABU91312	Abu91312	Novel	hum
487	5	62.5	255	6	ABU90405	Abu90405	Novel	hum
488	5	62.5	255	6	ABO09820	Abo09820	Human	sec
489	5	62.5	255	6	ABO11092	Abo11092	Human	sec
490	5	62.5	255	6	ABR71146	Abr71146	Human	sec
491	5	62.5	255	6	ABU87754	Abu87754	Human	PRO
492	5	62.5	255	6	ABU91622	Abu91622	Human	PRO
493	5	62.5	255	6	ABU84836	Abu84836	Human	sec
494	5	62.5	255	6	ABR69926	Abr69926	Human	sec
495	5	62.5	255	6	ABU80303	Abu80303	Human	PRO
496	5	62.5	255	6	ABU93572	Abu93572	Human	PRO
497	5	62.5	255	6	ABO10125	Abo10125	Human	sec
498	5	62.5	255	6	ABO09210	Abo09210	Human	sec
499	5	62.5	255	6	ABU10778	Abu10778	Human	sec
500	5	62.5	255	6	ABU95787	Abu95787	Human	PRO
501	5	62.5	255	6	ABU96996	Abu96996	Novel	hum
502	5	62.5	255	6	ABR70841	Abr70841	Human	sec
503	5	62.5	255	6	ABO05192	Abo05192	Novel	hum
504	5	62.5	255	6	ABO08600	Abo08600	Human	sec
505	5	62.5	255	6	ABO05807	Abo05807	Human	sec
506	5	62.5	255	6	ABR74196	Abr74196	Human	sec
507	5	62.5	255	6	ABR95788	Abr95788	Human	sec
508	5	62.5	255	6	ABR81085	Abr81085	Human	sec
509	5	62.5	255	6	ABR81390	Abr81390	Human	sec
510	5	62.5	255	6	ABM01086	Abm01086	Human	sec
511	5	62.5	255	6	ABR88688	Abr88688	Human	sec
512	5	62.5	255	6	ABM77509	Abm77509	Human	sec
513	5	62.5	255	6	ABO28993	Abo28993	Human	sec
514	5	62.5	255	6	ABO31738	Abo31738	Human	sec
515	5	62.5	255	6	ABM08155	Abm08155	Human	sec
516	5	62.5	255	6	ABO40635	Abo40635	Human	sec
517	5	62.5	255	6	ABO36060	Abo36060	Human	PRO
518	5	62.5	255	6	ABO44199	Abo44199	Human	PRO
519	5	62.5	255	6	ADA78290	Ada78290	Human	sec
520	5	62.5	255	6	ABM24994	Abm24994	Human	sec
521	5	62.5	255	6	ABO03262	Abo03262	Human	sec
522	5	62.5	255	6	ABR90518	Abr90518	Human	sec

523	5	62.5	255	6	ABM17432	Abm17432	Human	sec
524	5	62.5	255	6	ABR95178	Abr95178	Human	sec
525	5	62.5	255	6	ABR95483	Abr95483	Human	sec
526	5	62.5	255	6	ABO21721	Abo21721	Human	sec
527	5	62.5	255	6	ABR97985	Abr97985	Human	sec
528	5	62.5	255	6	ABR87773	Abr87773	Human	sec
529	5	62.5	255	6	ABM77814	Abm77814	Human	sec
530	5	62.5	255	6	ABM28044	Abm28044	Human	sec
531	5	62.5	255	6	ABM06325	Abm06325	Human	sec
532	5	62.5	255	6	ABM03831	Abm03831	Human	sec
533	5	62.5	255	6	ABM35282	Abm35282	Human	sec
534	5	62.5	255	6	ABM26519	Abm26519	Human	sec
535	5	62.5	255	6	ABO48301	Abo48301	Human	sec
536	5	62.5	255	6	ABR93043	Abr93043	Human	sec
537	5	62.5	255	6	ABO24804	Abo24804	Human	sec
538	5	62.5	255	6	ABM11815	Abm11815	Human	sec
539	5	62.5	255	6	ABM02916	Abm02916	Human	sec
540	5	62.5	255	6	ABM16212	Abm16212	Human	sec
541	5	62.5	255	6	ABO27773	Abo27773	Human	sec
542	5	62.5	255	6	ABM29264	Abm29264	Human	sec
543	5	62.5	255	6	ABM07240	Abm07240	Human	sec
544	5	62.5	255	6	ABM21334	Abm21334	Human	sec
545	5	62.5	255	6	ABM09680	Abm09680	Human	sec
546	5	62.5	255	6	ABO41550	Abo41550	Human	sec
547	5	62.5	255	6	ABO36365	Abo36365	Human	PRO
548	5	62.5	255	6	ABO43894	Abo43894	Human	PRO
549	5	62.5	255	6	ABM76594	Abm76594	Human	sec
550	5	62.5	255	6	ABM76290	Abm76290	Human	sec
551	5	62.5	255	6	ABM25909	Abm25909	Human	sec
552	5	62.5	255	6	ABM26214	Abm26214	Human	sec
553	5	62.5	255	6	ABO03567	Abo03567	Human	sec
554	5	62.5	255	6	ABO02652	Abo02652	Human	sec
555	5	62.5	255	6	ABR90823	Abr90823	Human	sec
556	5	62.5	255	6	ABR73891	Abr73891	Human	sec
557	5	62.5	255	6	ABO17143	Abo17143	Human	sec
558	5	62.5	255	6	ABR94568	Abr94568	Human	sec
559	5	62.5	255	6	ABR76075	Abr76075	Human	sec
560	5	62.5	255	6	ABR71451	Abr71451	Human	sec
561	5	62.5	255	6	ABR93348	Abr93348	Human	sec
562	5	62.5	255	6	ABR93653	Abr93653	Human	sec
563	5	62.5	255	6	ABR88078	Abr88078	Human	sec
564	5	62.5	255	6	ABO28078	Abo28078	Human	sec
565	5	62.5	255	6	ABO30213	Abo30213	Human	sec
566	5	62.5	255	6	ABO33422	Abo33422	Human	PRO
567	5	62.5	255	6	ABM05110	Abm05110	Human	sec
568	5	62.5	255	6	ABM09070	Abm09070	Human	sec
569	5	62.5	255	6	ABO36670	Abo36670	Human	sec
570	5	62.5	255	6	ABO35755	Abo35755	Human	PRO
571	5	62.5	255	6	ABO39720	Abo39720	Human	sec
572	5	62.5	255	6	ABM10595	Abm10595	Human	sec
573	5	62.5	255	6	ABM12120	Abm12120	Human	sec
574	5	62.5	255	6	ABO52266	Abo52266	Human	PRO
575	5	62.5	255	6	ABO52571	Abo52571	Human	PRO
576	5	62.5	255	6	ABO23889	Abo23889	Human	sec
577	5	62.5	255	6	ABR97375	Abr97375	Human	sec
578	5	62.5	255	6	ABR87163	Abr87163	Human	sec
579	5	62.5	255	6	ABM11205	Abm11205	Human	sec

580	5	62.5	255	6	ABM28349	Abm28349	Human	sec
581	5	62.5	255	6	ABO32348	AbO32348	Human	sec
582	5	62.5	255	6	ABM15475	Abm15475	Human	sec
583	5	62.5	255	6	ABM06630	Abm06630	Human	sec
584	5	62.5	255	6	ABM04441	Abm04441	Human	sec
585	5	62.5	255	6	ABM22554	Abm22554	Human	sec
586	5	62.5	255	6	ABM07850	Abm07850	Human	sec
587	5	62.5	255	6	ABO40940	AbO40940	Human	sec
588	5	62.5	255	6	ABM35587	Abm35587	Human	sec
589	5	62.5	255	6	ABM33350	Abm33350	Human	sec
590	5	62.5	255	6	ABO52876	AbO52876	Human	PRO
591	5	62.5	255	6	ABO50436	AbO50436	Human	sec
592	5	62.5	255	6	ABU99430	Abu99430	Human	sec
593	5	62.5	255	6	ABO04482	AbO04482	Human	sec
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596	5	62.5	255	6	ABR80780	AbR80780	Human	sec
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598	5	62.5	255	6	ABR88993	AbR88993	Human	sec
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644	5	62.5	255	6	ABO23196	Abo23196	Human	PRO
645	5	62.5	255	6	ABR92738	Abr92738	Human	sec
646	5	62.5	255	6	ABR81695	Abr81695	Human	sec
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709	5	62.5	255	6	ABO46105	Abo46105	Human	PRO
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719	5	62.5	255	7	ABO40025	Abo40025	Human	sec
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741	5	62.5	255	7	ABO49216	Abo49216	Human	sec
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762	5	62.5	255	7	ABO10647	Abo10647	Human	PRO
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767	5	62.5	255	7	ABM02001	Abm02001	Human	sec
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769	5	62.5	255	7	ABR90213	Abr90213	Human	sec
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773	5	62.5	255	7	ABM14255	Abm14255	Human	sec
774	5	62.5	255	7	ABM08460	Abm08460	Human	sec
775	5	62.5	255	7	ABO40330	Abo40330	Human	sec
776	5	62.5	255	7	ABM74765	Abm74765	Human	sec
777	5	62.5	255	7	ABM33960	Abm33960	Human	sec
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779	5	62.5	255	7	ABO48911	Abo48911	Human	sec
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781	5	62.5	255	7	ABO15618	Abo15618	Human	sec
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793	5	62.5	255	7	ABM15170	Abm15170	Human	sec
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797	5	62.5	255	7	ABM75375	Abm75375	Human	sec
798	5	62.5	255	7	ABM33655	Abm33655	Human	sec
799	5	62.5	255	7	ABO46410	Abo46410	Human	PRO
800	5	62.5	255	7	ADA82973	Ada82973	Human	sec
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804	5	62.5	255	7	ABM32314	Abm32314	Human	sec
805	5	62.5	255	7	ABM32619	Abm32619	Human	sec
806	5	62.5	255	7	ABM31704	Abm31704	Human	sec
807	5	62.5	255	7	ABM31094	Abm31094	Human	sec

808	5	62.5	255	7	ADD06011	Add06011	Human sec
809	5	62.5	255	8	ADE74675	Ade74675	Human sec
810	5	62.5	255	8	ADE75287	Ade75287	Human sec
811	5	62.5	258	3	AAG29883	Aag29883	Arabidops
812	5	62.5	276	6	ABP70958	Abp70958	Epoxide h
813	5	62.5	284	5	ABB06060	Abb06060	Human NS
814	5	62.5	284	6	ADA54082	Ada54082	Human pro
815	5	62.5	287	3	AAG48009	Aag48009	Arabidops
816	5	62.5	293	4	ABB71167	Abb71167	Drosophil
817	5	62.5	306	3	AAY71111	Aay71111	Human Hyd
818	5	62.5	306	4	AAM39918	Aam39918	Human pol
819	5	62.5	309	6	AAO27401	Aao27401	Human NSD
820	5	62.5	315	4	AAU08795	Aau08795	Human hyd
821	5	62.5	316	4	AAM41704	Aam41704	Human pol
822	5	62.5	319	2	AAW14075	Aaw14075	S.thermop
823	5	62.5	319	2	AAW22174	Aaw22174	S.thermop
824	5	62.5	327	3	AAG46298	Aag46298	Arabidops
825	5	62.5	328	7	ADC31068	Adc31068	Human nov
826	5	62.5	331	4	ABB58244	Abb58244	Drosophil
827	5	62.5	331	6	ABU44606	Abu44606	Protein e
828	5	62.5	332	4	ABB64061	Abb64061	Drosophil
829	5	62.5	333	3	AAB42014	Aab42014	Human ORF
830	5	62.5	333	6	ABM69430	Abm69430	Photorhab
831	5	62.5	341	2	AAW60800	Aaw60800	Deletion
832	5	62.5	343	5	ABB49365	Abb49365	Listeria
833	5	62.5	348	6	ABP99210	Abp99210	Orthosomy
834	5	62.5	350	4	AAU43404	Aau43404	Propionib
835	5	62.5	350	6	ABM39923	Abm39923	Propionib
836	5	62.5	350	6	ABU35933	Abu35933	Protein e
837	5	62.5	355	4	AAB61888	Aab61888	Soybean H
838	5	62.5	357	4	AAU35233	Aau35233	Enterococ
839	5	62.5	357	5	ABP41558	Abp41558	Human ova
840	5	62.5	357	6	ABU29266	Abu29266	Protein e
841	5	62.5	358	4	AAB61886	Aab61886	Soybean H
842	5	62.5	360	5	ABP39433	Abp39433	Staphyloc
843	5	62.5	361	5	ABP65988	Abp65988	Bifidobac
844	5	62.5	363	4	AAU58897	Aau58897	Propionib
845	5	62.5	363	6	ABM55416	Abm55416	Propionib
846	5	62.5	374	3	AAG14918	Aag14918	Arabidops
847	5	62.5	374	3	AAG46297	Aag46297	Arabidops
848	5	62.5	374	6	ABP78628	Abp78628	N. gonorr
849	5	62.5	379	6	ABU17000	Abu17000	Protein e
850	5	62.5	380	2	AAY06627	Aay06627	C. elegan
851	5	62.5	380	3	AAY84308	Aay84308	A tyrosyl
852	5	62.5	382	6	ABU42932	Abu42932	Protein e
853	5	62.5	388	4	AAB92746	Aab92746	Human pro
854	5	62.5	390	3	AAY91108	Aay91108	Staphyloc
855	5	62.5	390	3	AAY44710	Aay44710	S. pneumo
856	5	62.5	390	4	AAU34274	Aau34274	Staphyloc
857	5	62.5	390	6	ABR83207	Abr83207	S. aureus
858	5	62.5	390	6	ABR83206	Abr83206	S. aureus
859	5	62.5	390	6	ABU16084	Abu16084	Protein e
860	5	62.5	390	6	ABM71277	Abm71277	Staphyloc
861	5	62.5	392	4	AAU37130	Aau37130	Staphyloc
862	5	62.5	393	6	ABU43582	Abu43582	Protein e
863	5	62.5	394	5	ABP39989	Abp39989	Staphyloc
864	5	62.5	394	6	ABU42808	Abu42808	Protein e

865	5	62.5	395	4	AAB96543	Aab96543	Putative
866	5	62.5	397	6	ABU41189	Abu41189	Protein e
867	5	62.5	398	3	AAB26238	Aab26238	Streptoco
868	5	62.5	398	4	AAB60870	Aab60870	Mevalonat
869	5	62.5	398	6	ABU02204	Abu02204	S. pneumo
870	5	62.5	398	6	ABU97185	Abu97185	Enzyme po
871	5	62.5	399	3	AAB27153	Aab27153	T. pallid
872	5	62.5	399	6	ABU33730	Abu33730	Protein e
873	5	62.5	399	6	ABU48600	Abu48600	Protein e
874	5	62.5	399	6	ABU35711	Abu35711	Protein e
875	5	62.5	402	4	AAG81096	Aag81096	Mycobacte
876	5	62.5	402	4	ABB72058	Abb72058	Drosophil
877	5	62.5	402	6	ABU36402	Abu36402	Protein e
878	5	62.5	402	6	ABU34849	Abu34849	Protein e
879	5	62.5	402	7	ADD24624	Add24624	DNA polym
880	5	62.5	403	3	AAG14917	Aag14917	Arabidops
881	5	62.5	405	3	AAG50964	Aag50964	Arabidops
882	5	62.5	406	6	ABU31542	Abu31542	Protein e
883	5	62.5	407	4	ABB61414	Abb61414	Drosophil
884	5	62.5	411	4	ABB52847	Abb52847	Escherich
885	5	62.5	411	4	ABB69986	Abb69986	Drosophil
886	5	62.5	418	6	ABU48573	Abu48573	Protein e
887	5	62.5	422	5	ABB89714	Abb89714	Human pol
888	5	62.5	424	2	AAW89026	Aaw89026	Polypepti
889	5	62.5	424	4	ABB51126	Abb51126	Human sec
890	5	62.5	424	6	ABO45383	Abo45383	Novel hum
891	5	62.5	424	7	ABO26863	Abo26863	Protein a
892	5	62.5	425	6	ADA33581	Ada33581	Acinetoba
893	5	62.5	426	3	AAG29882	Aag29882	Arabidops
894	5	62.5	434	2	AAW60799	Aaw60799	Entire am
895	5	62.5	436	4	AAG99957	Aag99957	ERA bindi
896	5	62.5	436	6	AAO27403	Aao27403	Human NSD
897	5	62.5	442	3	AAG50963	Aag50963	Arabidops
898	5	62.5	442	6	ABU36187	Abu36187	Protein e
899	5	62.5	443	4	ABB70079	Abb70079	Drosophil
900	5	62.5	444	2	AAV55921	Aay55921	Pseudomon
901	5	62.5	446	3	AAG50962	Aag50962	Arabidops
902	5	62.5	446	5	ABG31356	Abg31356	Arabidops
903	5	62.5	446	5	ABG31357	Abg31357	Arabidops
904	5	62.5	446	5	ABG31358	Abg31358	Arabidops
905	5	62.5	448	3	AAV56047	Aay56047	Pseudomon
906	5	62.5	448	4	AAU36417	Aau36417	Pseudomon
907	5	62.5	448	6	ABU38728	Abu38728	Protein e
908	5	62.5	452	2	AAW95029	Aaw95029	A. niger
909	5	62.5	452	2	AAV00864	Aay00864	Cellobioh
910	5	62.5	467	3	AAG14916	Aag14916	Arabidops
911	5	62.5	467	3	AAG46296	Aag46296	Arabidops
912	5	62.5	469	2	AAW37881	Aaw37881	BRCA1 mod
913	5	62.5	469	2	AAV30149	Aay30149	Amino aci
914	5	62.5	470	5	AAE19854	Aae19854	Mouse TNF
915	5	62.5	476	4	ABB68156	Abb68156	Drosophil
916	5	62.5	481	3	AAB03415	Aab03415	Corn puta
917	5	62.5	481	6	ABR40707	Abr40707	Zea mays
918	5	62.5	497	6	ABU27337	Abu27337	Protein e
919	5	62.5	507	2	AAV37798	Aay37798	Protein i
920	5	62.5	509	4	ABB68905	Abb68905	Drosophil
921	5	62.5	511	5	ABP65798	Abp65798	Bifidobac

922	5	62.5	514	4	ABB62367	Abb62367	Drosophil
923	5	62.5	519	4	AAB90786	Aab90786	Human she
924	5	62.5	519	6	ABB99466	Abb99466	Amino aci
925	5	62.5	529	7	ADB70185	Adb70185	C. neofo
926	5	62.5	530	5	ABB53659	Abb53659	Lactococc
927	5	62.5	532	4	AAU36134	Aau36134	Klebsiell
928	5	62.5	532	4	AAU53526	Aau53526	Propionib
929	5	62.5	532	6	ABM50045	Abm50045	Propionib
930	5	62.5	533	6	ABU24808	Abu24808	Protein e
931	5	62.5	535	6	ABU23950	Abu23950	Protein e
932	5	62.5	539	4	AAB92520	Aab92520	Human pro
933	5	62.5	539	4	AAB92695	Aab92695	Human pro
934	5	62.5	539	4	AAM93969	Aam93969	Human sto
935	5	62.5	539	4	AAM93992	Aam93992	Human sto
936	5	62.5	568	3	AAAY15185	Aay15185	Partial s
937	5	62.5	569	3	AAG15474	Aag15474	Arabidops
938	5	62.5	571	6	ABM69952	Abm69952	Photorhab
939	5	62.5	574	3	AAG15473	Aag15473	Arabidops
940	5	62.5	579	4	AAB96740	Aab96740	Putative
941	5	62.5	591	4	AAU34826	Aau34826	E. coli c
942	5	62.5	591	4	AAG98955	Aag98955	E. coli g
943	5	62.5	591	6	ABU14765	Abu14765	Protein e
944	5	62.5	597	6	ABU48959	Abu48959	Protein e
945	5	62.5	603	4	ABG29655	Abg29655	Novel hum
946	5	62.5	604	3	AAB34841	Aab34841	Gene 42 h
947	5	62.5	606	6	ABJ25406	Abj25406	Aspergill
948	5	62.5	607	4	AAU38198	Aau38198	Salmonell
949	5	62.5	607	6	ABU47104	Abu47104	Protein e
950	5	62.5	607	6	ABU48135	Abu48135	Protein e
951	5	62.5	607	6	ABU31550	Abu31550	Protein e
952	5	62.5	607	6	ABU28078	Abu28078	Protein e
953	5	62.5	607	6	ABU50095	Abu50095	Protein e
954	5	62.5	608	5	ABB93507	Abb93507	Herbicida
955	5	62.5	614	4	AAB95229	Aab95229	Human pro
956	5	62.5	614	4	ABG24803	Abg24803	Novel hum
957	5	62.5	614	4	AAM94010	Aam94010	Human sto
958	5	62.5	616	5	ABB93900	Abb93900	Herbicida
959	5	62.5	618	4	AAG67089	Aag67089	Shiitake
960	5	62.5	619	3	AAG15472	Aag15472	Arabidops
961	5	62.5	621	3	AAG28040	Aag28040	Arabidops
962	5	62.5	623	3	AAG38774	Aag38774	Arabidops
963	5	62.5	627	2	AAW62553	Aaw62553	Protein o
964	5	62.5	627	2	AAW62552	Aaw62552	Shiitake
965	5	62.5	627	6	ABJ25460	Abj25460	Aspergill
966	5	62.5	635	2	AAAY24321	Aay24321	Mouse dep
967	5	62.5	637	4	AAM38980	Aam38980	Human pol
968	5	62.5	639	6	ABU35422	Abu35422	Protein e
969	5	62.5	640	4	ABB63959	Abb63959	Drosophil
970	5	62.5	649	6	ADB11640	Adb11640	Alloiococ
971	5	62.5	663	2	AAAY24322	Aay24322	Mouse dep
972	5	62.5	667	4	ABG10440	Abg10440	Novel hum
973	5	62.5	668	5	ABB93897	Abb93897	Herbicida
974	5	62.5	680	2	AAAY24320	Aay24320	Mouse dep
975	5	62.5	680	3	AAAY79196	Aay79196	Maize glu
976	5	62.5	691	5	ABB93681	Abb93681	Herbicida
977	5	62.5	693	3	AAAY56514	Aay56514	Human Jur
978	5	62.5	702	6	ABU19422	Abu19422	Protein e

979	5	62.5	712	4	AAB79540	Aab79540	Corynebac
980	5	62.5	714	6	ABM65388	Abm65388	Propionib
981	5	62.5	714	6	ABU24214	Abu24214	Protein e
982	5	62.5	718	5	ABB93899	Abb93899	Herbicida
983	5	62.5	719	4	ABB65541	Abb65541	Drosophil
984	5	62.5	727	3	AAG47308	Aag47308	Arabidops
985	5	62.5	731	3	AAG38773	Aag38773	Arabidops
986	5	62.5	734	4	ABB64014	Abb64014	Drosophil
987	5	62.5	739	2	AAR77501	Aar77501	Malate sy
988	5	62.5	739	4	AAB79539	Aab79539	Corynebac
989	5	62.5	739	4	AAG93234	Aag93234	C glutami
990	5	62.5	739	7	ADD13393	Add13393	C. glutam
991	5	62.5	753	5	ABB48026	Abb48026	Listeria
992	5	62.5	762	6	ABJ26060	Abj26060	Aspergill
993	5	62.5	763	6	ABU20715	Abu20715	Protein e
994	5	62.5	783	5	ABP35616	Abp35616	Fungal ZB
995	5	62.5	784	4	ABG30180	Abg30180	Novel hum
996	5	62.5	786	4	ABG09526	Abg09526	Novel hum
997	5	62.5	788	6	ABU45872	Abu45872	Protein e
998	5	62.5	796	5	ABP73364	Abp73364	Candida a
999	5	62.5	815	6	ABU38957	Abu38957	Protein e
1000	5	62.5	819	6	ABU49933	Abu49933	Protein e

ALIGNMENTS

RESULT 1

AAAY94771

ID AAY94771 standard; protein; 8 AA.

XX

AC AAY94771;

XX

DT 12-FEB-2001 (first entry)

XX

DE Beta-secretase substrate peptide SEQ ID 17.

XX

KW Beta-secretase; enzyme; amyloid plaque; Alzheimer's disease;

KW Down's syndrome; amyloid angiopathy; gene therapy; neuroprotective.

XX

OS Synthetic.

XX

PN WO200058479-A1.

XX

PD 05-OCT-2000.

XX

PF 23-MAR-2000; 2000WO-US007755.

XX

PR 26-MAR-1999; 99US-00277229.

XX

PA (AMGE-) AMGEN INC.

XX

PI Citron M, Vassar RJ, Bennett BD;

XX

DR WPI; 2000-594643/56.

XX

PT Isolated beta-secretase nucleic acids and encoded polypeptides, useful

PT for diagnosis and gene therapy of Alzheimer's disease.

XX

PS Example 10; Page 117; 145pp; English.

XX

CC This invention relates to 3 nucleotide sequences encoding beta-secretase
CC proteins. Beta-secretase is an enzyme involved in the production of one
CC of the components of amyloid plaques involved in Alzheimer's disease. The
CC invention includes an expression vector comprising the nucleotide
CC sequence, a host cell comprising the expression vector, and a process for
CC producing the protein through culturing the transformed cells. Also
CC included in the invention are a polypeptide derivative of the beta-
CC secretase protein, a fusion protein comprising beta-secretase fused to a
CC heterologous amino acid sequence, and a method for modulating the levels
CC of beta-secretase polypeptide in a mammal comprising administering the
CC polynucleotide sequence. Beta-secretase exhibits neuroprotective and
CC nootropic activity. The beta-secretase nucleotide sequence may be used to
CC map locations of the beta-secretase gene and related genes on chromosomes
CC and as hybridization probes in diagnostic assays to test for the presence
CC of beta-secretase DNA or RNA, such as in Alzheimer's disease, Down's
CC syndrome, and amyloid angiopathy. The nucleotide sequence may also be
CC used as anti-sense inhibitors of beta-secretase expression, in gene
CC therapy of Alzheimer's disease, and for the identification of compounds
CC that modulate beta-secretase activity. Antibodies to the beta-secretase
CC protein may be used for in vitro and in vivo diagnostic purposes to
CC detect the presence of beta-secretase polypeptide in a body fluid or cell
CC sample. The present sequence represents a beta-secretase substrate
CC peptide

XX

SQ Sequence 8 AA;

Query Match 100.0%; Score 8; DB 3; Length 8;

Best Local Similarity 100.0%; Pred. No. 1.4e+06;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVNLDAEF 8

|||||||

Db 1 EVNLDAEF 8

RESULT 2

AAE10661

ID AAE10661 standard; peptide; 8 AA.

XX

AC AAE10661;

XX

DT 10-DEC-2001 (first entry)

XX

DE Human aspartyl protease-1 beta-secretase Swedish mutant peptide.

XX

KW Human; aspartyl protease 1; Aspl; amyloid precursor protein; APP;

KW Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;

KW amyloid plaque; neuronal loss; proteolytic; nootropic; neuroprotective;

KW aspartyl protease-1 beta-secretase Swedish mutant peptide.

XX

OS Homo sapiens.

OS Synthetic.

XX

FH Key Location/Qualifiers
FT Cleavage-site 4. .5

XX

PN GB2357767-A.

XX

PD 04-JUL-2001.

XX

PF 22-SEP-2000; 2000GB-00023315.

XX

PR 23-SEP-1999; 99US-00404133.

PR 23-SEP-1999; 99US-0155493P.

PR 23-SEP-1999; 99WO-US020881.

PR 13-OCT-1999; 99US-00416901.

PR 06-DEC-1999; 99US-0169232P.

XX

PA (PHAA) PHARMACIA & UPJOHN CO.

XX

PI Bienkowski MJ, Gurney M;

XX

DR WPI; 2001-444208/48.

XX

PT Polypeptide comprising fragments of human aspartyl protease with amyloid
PT precursor protein processing activity and alpha-secretase activity, for
PT identifying modulators useful in treating Alzheimer's disease.

XX

PS Example 15; Page 92; 187pp; English.

XX

CC The patent discloses human aspartyl protease 1 (hu-Asp1) or modified Asp1
CC proteins which lack transmembrane domain or amino terminal domain or
CC cytoplasmic domain and retains alpha-secretase activity and amyloid
CC protein precursor (APP) processing activity. The proteins of the
CC invention are useful for assaying hu-Asp1 alpha-secretase activity, which
CC in turn is useful for identifying modulators of hu-Asp1 alpha-secretase
CC activity, where modulators that increase hu-Asp1 alpha-secretase activity
CC are useful for treating Alzheimer's disease (AD) which causes progressive
CC dementia with consequent formation of amyloid plaques, neurofibrillary
CC tangles, gliosis and neuronal loss. Hu-Asp1 protease substrate is useful
CC for assaying hu-Asp1 proteolytic activity, by contacting hu-Asp1 protein
CC with the substrate under acidic conditions and determining the level of
CC hu-Asp1 proteolytic activity. The present sequence is human aspartyl
CC protease-1 (hu-Asp-1) beta-secretase Swedish (Sw) mutant peptide which is
CC used for determining the enzymatic activity of Asp-1 protein lacking a
CC transmembrane (TM) domain and containing (His)6 tag

XX

SQ Sequence 8 AA;

Query Match 100.0%; Score 8; DB 4; Length 8;

Best Local Similarity 100.0%; Pred. No. 1.4e+06;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAEF 8

|||||||

Db 1 EVNLDAEF 8

RESULT 3

AAE02613

ID AAE02613 standard; peptide; 8 AA.
 XX
 AC AAE02613;
 XX
 DT 10-AUG-2001 (first entry)
 XX
 DE Human Aspartyl protease-1 beta-secretase Swedish mutant form peptide.
 XX
 KW Human; alpha-secretase; amyloid precursor protein; APP; therapy;
 KW Alzheimer's disease; antialzheimer's; aspartyl protease 1; Aspl;
 KW beta-secretase.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Cleavage-site 4. .5
 XX
 PN WO200123533-A2.
 XX
 PD 05-APR-2001.
 XX
 PF 22-SEP-2000; 2000WO-US026080.
 XX
 PR 23-SEP-1999; 99US-0155493P.
 PR 23-SEP-1999; 99WO-US020881.
 PR 13-OCT-1999; 99US-00416901.
 PR 06-DEC-1999; 99US-0169232P.
 XX
 PA (PHAA) PHARMACIA & UPJOHN CO.
 XX
 PI Gurney M, Bienkowski MJ;
 XX
 DR WPI; 2001-290516/30.
 XX
 PT Enzymes that cleave the alpha-secretase site of the amyloid precursor
 PT protein, useful for the treatment of Alzheimer's disease.
 XX
 PS Example 15; Page 94; 189pp; English.
 XX
 CC The present invention relates to enzymes for cleaving the alpha-
 CC secretase site of the amyloid precursor protein (APP) and methods of
 CC identifying those enzymes. The methods may be used to identify enzymes
 CC that may be used to cleave the alpha-secretase cleavage site of the APP
 CC protein. The enzymes may be used to treat or modulate the progress of
 CC Alzheimer's disease. The present sequence is human Aspartyl protease-1
 CC (hu-Asp-1) beta-secretase, Swedish (Sw) mutant form peptide which is used
 CC for determining the enzymatic activity of Asp-1 deltaTM (His)6 protein
 XX
 SQ Sequence 8 AA;

Query Match 100.0%; Score 8; DB 4; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVNLDAEF 8
 |||||
 Db 1 EVNLDAEF 8

RESULT 4

ABB78622

ID ABB78622 standard; peptide; 8 AA.

XX

AC ABB78622;

XX

DT 16-JUL-2002 (first entry)

XX

DE Human beta secretase peptide SEQ ID NO:71.

XX

KW Human; Asp-1; Asp-2; aspartyl protease; Alzheimer's disease; proteolytic.

XX

OS Homo sapiens.

XX

PN GB2367060-A.

XX

PD 27-MAR-2002.

XX

PF 29-OCT-2001; 2001GB-00025934.

XX

PR 23-SEP-1999; 99US-00404133.

PR 23-SEP-1999; 99US-0155493P.

PR 23-SEP-1999; 99WO-US020881.

PR 13-OCT-1999; 99US-00416901.

PR 06-DEC-1999; 99US-0169232P.

PR 22-SEP-2000; 2000GB-00023315.

XX

PA (PHAA) PHARMACIA & UPJOHN CO.

XX

PI Bienkowski MJ, Gurney M;

XX

DR WPI; 2002-397167/43.

XX

PT Human aspartyl protease 1 substrates useful in assays to detect aspartyl
PT protease activity, e.g. for the diagnosis of Alzheimer's disease.

XX

PS Example 15; Page 92; 182pp; English.

XX

CC The present invention describes a human aspartyl protease 1 (hu-Asp1)
CC substrate (I) which comprises a peptide of no more than 50 amino acids,
CC and which comprises the 8 amino acid sequence Gly-Leu-Ala-Leu-Ala-Leu-
CC Glu-Pro. Also described are: (1) a method (II) for assaying hu-Asp1
CC proteolytic activity, comprising: (a) contacting a hu-Asp1 protein with
CC (I) under acidic conditions; and (b) determining the level of hu-Asp1
CC proteolytic activity; (2) a purified polynucleotide (III) comprising a
CC nucleotide sequence that hybridises under stringent conditions to the non
CC -coding strand complementary to a defined 1804 nucleotide sequence (see
CC ABL52456) where the nucleotide sequence encodes a polypeptide having Asp1
CC proteolytic activity and lacks nucleotides encoding a transmembrane
CC domain); (3) a purified polynucleotide (III') comprising a sequence that
CC hybridises under stringent conditions to (III) (the nucleotide sequence
CC encodes a polypeptide further lacking a pro-peptide domain corresponding
CC to amino acids 23-62 of hu-Asp1 (see ABB78589)); (4) a vector (IV)
CC comprising (III) or (III'); and (5) a host cell (V) transformed or
CC transfected with (III), (III') and/or (IV). The hu-Asp1 protease

CC substrate (I) may be used as an enzyme substrate in assays to detect
CC aspartyl protease activity, (II) and therefore diagnose diseases
CC associated with aberrant hu-Asp1 expression and activity such as
CC Alzheimer's disease. Hu-Asp1 has been localised to chromosome 21, while
CC hu-Asp2 has been localised to chromosome 11q23.3-24.1. The present
CC sequence represents a human beta secretase peptide, which is used in an
CC example from the present invention
XX
SQ Sequence 8 AA;

Query Match 100.0%; Score 8; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAEF 8
| | | | | | | |
Db 1 EVNLDAEF 8

RESULT 5

ABR54159

ID ABR54159 standard; peptide; 8 AA.

XX

AC ABR54159;

XX

DT 19-JUN-2003 (first entry)

XX

DE Beta-secretase substrate peptide #257.

XX

KW Beta-secretase; nootropic; neuroprotective; Secretase Inhibitor Beta;
KW substrate; beta-APP; amyloid precursor protein; Alzheimer's disease;
KW amyloid beta peptide deposition; Down's syndrome.

XX

OS Synthetic.

XX

PN WO200294985-A2.

XX

PD 28-NOV-2002.

XX

PF 17-MAY-2002; 2002WO-US015590.

XX

PR 22-MAY-2001; 2001US-0292591P.

PR 30-AUG-2001; 2001US-0316115P.

XX

PA (MERI) MERCK & CO INC.

XX

PI Bruce JE, Tang X, Garsky V, Brady SF, Li Y, Chen-Dodson E;
PI Sardana M, Shafer JA;

XX

DR WPI; 2003-148462/14.

XX

PT New beta-secretase substrate peptides, useful as substrates in assays for
PT measuring beta-secretase activity, or for screening test compounds for
PT the ability to inhibit beta-secretase activity used for treating
PT Alzheimer's disease.

XX

PS Example 2; Fig 1; 103pp; English.

XX
 CC The invention relates to a novel substantially pure beta-secretase
 CC substrate peptide. A peptide of the invention has nootropic, and
 CC neuroprotective activity. The peptide acts as a Secretase Inhibitor Beta.
 CC The beta-secretase substrate peptides are useful as substrates in various
 CC assays for measuring beta-secretase activity. The methods are useful for
 CC screening test compounds for the ability to inhibit beta-secretase
 CC activity, or inhibiting the cleavage of beta-APP (amyloid precursor
 CC protein) in mammalian hosts, which can be used for treating conditions
 CC related to amyloid beta peptide deposition, e.g. Alzheimer's disease or
 CC Down's syndrome. The present sequence represents a beta secretase
 CC substrate peptide of the invention

XX

SQ Sequence 8 AA;

Query Match 100.0%; Score 8; DB 6; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAEF 8
 |||||
 Db 1 EVNLDAEF 8

RESULT 6

AAW82081

ID AAW82081 standard; peptide; 9 AA.

XX

AC AAW82081;

XX

DT 18-FEB-1999 (first entry)

XX

DE Fluorogenic protease indicator protease binding peptide #59.

XX

KW Protease activity; fluorophore; detection; fluorogenic; cellular uptake;
 KW conformation change.

XX

OS Synthetic.

XX

PN WO9837226-A1.

XX

PD 27-AUG-1998.

XX

PF 20-FEB-1998; 98WO-US003000.

XX

PR 20-FEB-1997; 97US-00802981.

XX

PA (ONCO-) ONCOIMMUNIN INC.

XX

PI Komoriya A, Packard BS;

XX

DR WPI; 1998-467579/40.

XX

PT New fluorogenic compositions - containing 2 fluorophores separated by a
 PT peptide comprising a protease binding site, used for detecting protease
 PT activity in samples.

XX

PS Claim 4; Page 77; 90pp; English.
 XX
 CC AAW82023-W82240 are peptides used in the construction of a fluorogenic
 CC composition which is used for the detection of protease activity in
 CC biological samples. The products can be used for the detection of
 CC conformation changes in nucleic acids, oligosaccharides, polysaccharides,
 CC proteins, peptides, lipids, phospholipids, glycolipids, glycoproteins,
 CC steroids or polymers. In addition, attachment of a hydrophobic group to a
 CC molecule can be used to enhance uptake by cells. The composition is
 CC composed of P = peptide comprising a protease binding site for the
 CC protease, F1, F2 peptides = fluorophores where F1 is attached to the
 CC amino terminal amino acid and F2 is attached to the carboxyl terminal
 CC amino acid and S1, S2 peptides = when present, are peptide spacers where
 CC S1, when present, is attached to the amino terminal acid, and S2, when
 CC present, is attached to the carboxyl terminal amino acid
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 8; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAEF 8
 |||||
 Db 2 EVNLDAEF 9

RESULT 7

AAB07874

ID AAB07874 standard; peptide; 9 AA.

XX

AC AAB07874;

XX

DT 14-NOV-2000 (first entry)

XX

DE A peptide fragment derived from beta-amyloid precursor protein.

XX

KW Beta-secretase; beta-amyloid precursor protein; beta-amyloid peptide;

KW amyloid plaque component; Alzheimer's disease; amyloidogenic disease;

KW inhibitor.

XX

OS Homo sapiens.

XX

PN WO200047618-A2.

XX

PD 17-AUG-2000.

XX

PF 10-FEB-2000; 2000WO-US003819.

XX

PR 10-FEB-1999; 99US-0119571P.

PR 15-JUN-1999; 99US-0139172P.

XX

PA (ELAN-) ELAN PHARM INC.

XX

PI Anderson JP, Basi G, Doane MT, Frigon N, John V, Power M;

PI Sinha S, Tatsuno G, Tung J, Wang S, Mcconlogue L;

XX

DR WPI; 2000-533011/48.
 XX
 PT Purified beta-secretase protein used in assays to discover inhibitors
 PT which can be used for the treatment of amyloidogenic diseases e.g.
 PT Alzheimer's disease.
 XX
 PS Disclosure; Page 12; 121pp; English.
 XX
 CC The specification describes a beta-secretase enzyme. The enzyme cleaves
 CC beta-amyloid precursor protein to produce beta-amyloid peptide. This
 CC enzyme is therefore implicated in the production of amyloid plaque
 CC components which accumulate in the brains of individuals afflicted with
 CC Alzheimer's disease. Inhibitors of beta-secretase are administered to a
 CC mammalian subject e.g. with Alzheimer's disease or Alzheimer's disease-
 CC like pathology to test if they maintain or improve cognitive ability or
 CC reduce the plaque burden. The compounds are used for the treatment of
 CC amyloidogenic diseases e.g. Alzheimer's disease. The present sequence
 CC represents a peptide derived from beta-amyloid precursor protein
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 8; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAEF 8
 |||||
 Db 2 EVNLDAEF 9

RESULT 8

AAB07894

ID AAB07894 standard; peptide; 9 AA.

XX

AC AAB07894;

XX

DT 14-NOV-2000 (first entry)

XX

DE Substrate for beta-secretase enzyme.

XX

KW Beta-secretase; beta-amyloid precursor protein; beta-amyloid peptide;
 KW amyloid plaque component; Alzheimer's disease; amyloidogenic disease;
 KW inhibitor.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Cleavage-site 5. .6

XX

PN WO200047618-A2.

XX

PD 17-AUG-2000.

XX

PF 10-FEB-2000; 2000WO-US003819.

XX

PR 10-FEB-1999; 99US-0119571P.

PR 15-JUN-1999; 99US-0139172P.

XX
 PA (ELAN-) ELAN PHARM INC.
 XX
 PI Anderson JP, Basi G, Doane MT, Frigon N, John V, Power M;
 PI Sinha S, Tatsuno G, Tung J, Wang S, Mcconlogue L;
 XX
 DR WPI; 2000-533011/48.
 XX
 PT Purified beta-secretase protein used in assays to discover inhibitors
 PT which can be used for the treatment of amyloidogenic diseases e.g.
 PT Alzheimer's disease.
 XX
 PS Example 4; Page 71; 121pp; English.
 XX
 CC The specification describes a beta-secretase enzyme. The enzyme cleaves
 CC beta-amyloid precursor protein to produce beta-amyloid peptide. This
 CC enzyme is therefore implicated in the production of amyloid plaque
 CC components which accumulate in the brains of individuals afflicted with
 CC Alzheimer's disease. Inhibitors of beta-secretase are administered to a
 CC mammalian subject e.g. with Alzheimer's disease or Alzheimer's disease-
 CC like pathology to test if they maintain or improve cognitive ability or
 CC reduce the plaque burden. The compounds are used for the treatment of
 CC amyloidogenic diseases e.g. Alzheimer's disease. The present sequence
 CC represents a peptide substrate used to test the activity of beta-
 CC secretase enzyme
 XX
 SQ Sequence 9 AA;

 Query Match 100.0%; Score 8; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 EVNLDAEF 8
 |||||
 Db 2 EVNLDAEF 9

 RESULT 9
 AAG73297
 ID AAG73297 standard; peptide; 9 AA.
 XX
 AC AAG73297;
 XX
 DT 14-AUG-2001 (first entry)
 XX
 DE Protease indicator compound peptide #26.
 XX
 KW Protease detection; peptide cleavage; enzyme activity; fluorogenic;
 KW viral infection; cancer metastasis; emphysema; arthritis; thrombosis;
 KW haemophilia.
 XX
 OS Synthetic.
 XX
 PN WO200118238-A1.
 XX
 PD 15-MAR-2001.
 XX

PF 11-SEP-2000; 2000WO-US024882.

XX

PR 10-SEP-1999; 99US-00394019.

XX

PA (ONCO-) ONCOIMMUNIN INC.

XX

PI Komoriya A, Packard BS;

XX

DR WPI; 2001-389573/41.

XX

PT New fluorogenic compositions whose fluorescence level increases in the
PT presence of active proteases, useful for detecting and localizing
PT protease activity in biological samples, particularly in frozen tissue
PT samples.

XX

PS Claim 1; Page 70; 86pp; English.

XX

CC The present invention describes fluorogenic compositions which can be
CC used for the detection of protease activity. This can be useful as an
CC indicator of viral infection, cancer metastasis, haemophilia, emphysema,
CC thrombosis and arthritis. The fluorogenic compositions comprise a
CC peptide, a peptide spacer and a donor and an acceptor fluorophore. The
CC peptide is cleaved by a protease and the fluorophores can then be
CC detected. The present sequence is one of the peptides described in the
CC exemplification of the invention

XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 8; DB 4; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.4e+06;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAEF 8

|||||||

Db 2 EVNLDAEF 9

RESULT 10

ABB06519

ID ABB06519 standard; peptide; 9 AA.

XX

AC ABB06519;

XX

DT 31-MAY-2002 (first entry)

XX

DE Beta-secretase related peptide SEQ ID NO:113.

XX

KW Beta-secretase; enzyme; cleavage site; amyloid protein precursor; APP;
KW aspartyl protease; neuroprotective; nootropic; beta-secretase inhibitor;
KW Alzheimer's disease.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN WO200206306-A2.

XX

PD 24-JAN-2002.

XX
PF 19-JUL-2001; 2001WO-US023035.
XX
PR 19-JUL-2000; 2000US-0219795P.
PR 12-MAR-2001; 2001US-0275251P.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Yan R, Tomasselli AG, Gurney ME, Emmons TL, Bienkowski MJ;
PI Heinrikson RL;
XX
DR WPI; 2002-216995/27.
XX
PT Novel substrates for human aspartyl protease useful for identifying
PT modulators of beta secretase activity of aspartyl protease for treating
PT Alzheimer's disease.
XX
PS Disclosure; Page 156; 188pp; English.
XX
CC The present invention describes an isolated peptide (I) comprising a
CC sequence of at least four amino acids, where the peptide is a substrate
CC for conducting aspartyl protease assays. (I) has neuroprotective and
CC nootropic activities, and can be used as an inhibitor of beta-secretase
CC activity. A beta-secretase modulator from the present invention can be
CC used for inhibiting beta-secretase activity in vivo, and in the
CC manufacture of a medicament for the treatment of Alzheimer's disease.
CC Pharmaceutical compositions from the present invention can be used for
CC treating a disease or condition characterised by an abnormal beta-
CC secretase activity. (I) is useful for identifying agents that modulate
CC the activity of human Asp2 aspartyl protease (Hu-Asp2). (I) is useful as
CC a core structure to construct derivatives. ABL49914 to ABL49925 and
CC ABB06409 to ABB06593 represent sequences used in the exemplification of
CC the present invention
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 8; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAEF 8
| | | | | | | |
Db 1 EVNLDAEF 8

RESULT 11

ABB09003

ID ABB09003 standard; peptide; 9 AA.

XX

AC ABB09003;

XX

DT 19-JUN-2002 (first entry)

XX

DE Peptide #1 used as a tag to identify cleavage products.

XX

KW Amyloid precursor protein; APP; Alzheimer's disease; nootropic;
KW neuroprotective; cerebroprotective; haemostatic; antiparkinsonian;

KW Down's syndrome; cerebral amyloid angiopathy; dementia.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Cleavage-site 5. .6
 FT /note= "Beta secretase cleavage site"
 XX
 PN WO200202505-A2.
 XX
 PD 10-JAN-2002.
 XX
 PF 29-JUN-2001; 2001WO-US020852.
 XX
 PR 30-JUN-2000; 2000US-0215323P.
 XX
 PA (ELAN-) ELAN PHARM INC.
 XX
 PI Fang LY, Hom R, John V, Maillaire M;
 XX
 DR WPI; 2002-171625/22.
 XX
 PT New substituted amines are e.g. beta-amyloid peptide inhibitors, useful
 PT for treating Alzheimer's disease, mild cognitive impairment and Down's
 PT syndrome.
 XX
 PS Example D; Page 96; 136pp; English.
 XX
 CC This invention relates to substituted amines and their salts, which are
 CC nootropic, neuroprotective, cerebroprotective, haemostatic and
 CC antiparkinsonian in their action. They are used in the preparation of a
 CC composition useful for treating, preventing or delaying the on-set of
 CC Alzheimer's disease, for treating mild cognitive impairment, Down's
 CC syndrome, cerebral amyloid angiopathy, dementia associated with
 CC Parkinson's disease, dementia associated with progressive supranuclear
 CC palsy, and dementia associated with cortical basal degeneration. They are
 CC also useful for treating diseases characterised by beta-amyloid deposits
 CC in brain, and for producing beta-secretase complexes. This sequence
 CC represents a peptide that incorporate the known cleavage site of beta-
 CC secretase. This substrate is used to assay beta-secretase activity
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 8; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAEF 8
 |||||
 Db 2 EVNLDAEF 9

RESULT 12
 ABU60429
 ID ABU60429 standard; peptide; 9 AA.
 XX
 AC ABU60429;

XX
 DT 29-APR-2003 (first entry)
 XX
 DE Protease binding peptide motif SEQ ID 139.
 XX
 KW Protease; indicator; chromophore; H-dimer; fluorescence; absorbance;
 KW nuclease; screening; fluorophore; substrate cleavage.
 XX
 OS Synthetic.
 XX
 PN WO200261038-A2.
 XX
 PD 08-AUG-2002.
 XX
 PF 21-DEC-2001; 2001WO-US049781.
 XX
 PR 22-DEC-2000; 2000US-00747287.
 XX
 PA (ONCO-) ONCOIMMUNIN INC.
 XX
 PI Packard BS, Komoriya A;
 XX
 DR WPI; 2002-698548/75.
 XX
 PT Indicator composition comprising polypeptide or nucleic acid backbone
 PT joining two same chromophores resulting in quenching of fluorescence
 PT of/change in absorbance of chromophores, useful for detecting protease
 PT activity.
 XX
 PS Disclosure; Page 34; 97pp; English.
 XX
 CC This invention describes a novel indicator composition (referred as homo-
 CC doubly labeled compositions) comprising a polypeptide backbone or a
 CC nucleic acid backbone joining two chromophores of the same species
 CC whereby the chromophores form an H-dimer resulting in quenching of the
 CC fluorescence of or a change in the absorbance of the chromophore, a
 CC decrease in fluorescence or a change in absorbance indicates that the
 CC first molecule and the second molecule are interacting. The indicator is
 CC useful for detecting the activity of a protease, where an increase in
 CC fluorescence or a change in absorbance indicates that the protease
 CC cleaves the polypeptide backbone. The indicator is attached to a solid
 CC support inside a mammalian, yeast or insect cell. The composition bears a
 CC hydrophobic group such as Fmoc, 9-fluoreneacetyl group, 1-
 CC fluorene-carboxylic group, 9-fluorene-carboxylic group, and 9-fluorenone-1-
 CC carboxylic group, benzyloxycarbonyl, Xanthyl (Xan), Trityl (Trt), 4-
 CC methyltrityl (Mtt), 4-methoxytrityl (Mmt), 4-methoxy-2,3, 6-trimethyl-
 CC benzenesulphonyl (Mtr), Mesitylene-2-sulphonyl (Mts), 4,4'-
 CC dimethoxybenzhydryl (Mbh), etc. The method described in the invention is
 CC useful for detecting protease or nuclease activity (or the presence of
 CC nucleic acid) in histological section, cells in culture, (e.g., seeded or
 CC cultured adherent cells), a biological sample such as tissue, biopsy,
 CC lymph, embryo, or whole animal, or cell suspension derived from a
 CC biological sample such as tissue, blood, urine, saliva, lymph, or biopsy.
 CC The indicator composition is also useful for screening a test agent for
 CC the ability to modulate a protease (or a nuclease, lipase, etc.). The
 CC indicator reagents allow rapid determination of protease activity in a
 CC matter of minutes in a single-step procedure. The fluorescent indicators

CC both absorb and emit in the visible range (400-800 nm). These signals are
CC therefore not readily quenched by, nor is activation of the fluorophores,
CC that is, absorption of light, interfered with by background molecules;
CC therefore they are easily detected in biological samples. The fluorogenic
CC protease indicators utilise high efficiency fluorophores and are able to
CC achieve a high degree of quenching while providing a strong signal when
CC the quench is released by cleavage of the peptide substrate. The high
CC signal allows detection of very low levels of protease activity. Thus the
CC fluorogenic protease indicators are particularly well suited for in situ
CC detection of protease activity. ABU60357-ABU60477 represent peptides use
CC to illustrate the method described in the disclosure of the invention

XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 8; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAEF 8
| | | | | | | |
Db 2 EVNLDAEF 9

RESULT 13

ABU60441

ID ABU60441 standard; peptide; 9 AA.

XX

AC ABU60441;

XX

DT 29-APR-2003 (first entry)

XX

DE Protease binding peptide motif SEQ ID 165.

XX

KW Protease; indicator; chromophore; H-dimer; fluorescence; absorbance;
KW nuclease; screening; fluorophore; substrate cleavage.

XX

OS Synthetic.

XX

PN WO200261038-A2.

XX

PD 08-AUG-2002.

XX

PF 21-DEC-2001; 2001WO-US049781.

XX

PR 22-DEC-2000; 2000US-00747287.

XX

PA (ONCO-) ONCOIMMUNIN INC.

XX

PI Packard BS, Komoriya A;

XX

DR WPI; 2002-698548/75.

XX

PT Indicator composition comprising polypeptide or nucleic acid backbone
PT joining two same chromophores resulting in quenching of fluorescence
PT of/change in absorbance of chromophores, useful for detecting protease
PT activity.

XX

PS Disclosure; Page 35; 97pp; English.

XX

CC This invention describes a novel indicator composition (referred as homo-
CC doubly labeled compositions) comprising a polypeptide backbone or a
CC nucleic acid backbone joining two chromophores of the same species
CC whereby the chromophores form an H-dimer resulting in quenching of the
CC fluorescence of or a change in the absorbance of the chromophore, a
CC decrease in fluorescence or a change in absorbance indicates that the
CC first molecule and the second molecule are interacting. The indicator is
CC useful for detecting the activity of a protease, where an increase in
CC fluorescence or a change in absorbance indicates that the protease
CC cleaves the polypeptide backbone. The indicator is attached to a solid
CC support inside a mammalian, yeast or insect cell. The composition bears a
CC hydrophobic group such as Fmoc, 9-fluoreneacetyl group, 1-
CC fluorene-carboxylic group, 9-fluorene-carboxylic group, and 9-fluorenone-1-
CC carboxylic group, benzyloxycarbonyl, Xanthyl (Xan), Trityl (Trt), 4-
CC methyltrityl (Mtt), 4-methoxytrityl (Mmt), 4-methoxy-2,3, 6-trimethyl-
CC benzenesulphonyl (Mtr), Mesitylene-2-sulphonyl (Mts), 4,4'-
CC dimethoxybenzhydryl (Mbh), etc. The method described in the invention is
CC useful for detecting protease or nuclease activity (or the presence of
CC nucleic acid) in histological section, cells in culture, (e.g., seeded or
CC cultured adherent cells), a biological sample such as tissue, biopsy,
CC lymph, embryo, or whole animal, or cell suspension derived from a
CC biological sample such as tissue, blood, urine, saliva, lymph, or biopsy.
CC The indicator composition is also useful for screening a test agent for
CC the ability to modulate a protease (or a nuclease, lipase, etc.). The
CC indicator reagents allow rapid determination of protease activity in a
CC matter of minutes in a single-step procedure. The fluorescent indicators
CC both absorb and emit in the visible range (400-800 nm). These signals are
CC therefore not readily quenched by, nor is activation of the fluorophores,
CC that is, absorption of light, interfered with by background molecules;
CC therefore they are easily detected in biological samples. The fluorogenic
CC protease indicators utilise high efficiency fluorophores and are able to
CC achieve a high degree of quenching while providing a strong signal when
CC the quench is released by cleavage of the peptide substrate. The high
CC signal allows detection of very low levels of protease activity. Thus the
CC fluorogenic protease indicators are particularly well suited for in situ
CC detection of protease activity. ABU60357-ABU60477 represent peptides use
CC to illustrate the method described in the disclosure of the invention

XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 8; DB 5; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.4e+06;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVNLDAEF 8

|||||||

Db 2 EVNLDAEF 9

RESULT 14

AAE16663

ID AAE16663 standard; peptide; 9 AA.

XX

AC AAE16663;

XX

DT 09-APR-2002 (first entry)
 XX
 DE Oligopeptide substrate #1, used in the assay of the invention.
 XX
 KW Disubstituted amine derivative; Alzheimer's disease; Down's syndrome;
 KW degenerative disease; beta-amyloid deposit; mild cognitive impairment;
 KW hereditary cerebral haemorrhage; amyloidosis; degenerative dementia;
 KW cerebral amyloid angiopathy; Parkinson's disease; supranuclear palsy;
 KW cortical basal degeneration; AD; MCI; amyloid precursor protein;
 KW beta-secretase; amyloid beta peptide; A beta peptide.
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT Cleavage-site 5. .6
 XX
 PN WO200202518-A2.
 XX
 PD 10-JAN-2002.
 XX
 PF 29-JUN-2001; 2001WO-US020856.
 XX
 PR 30-JUN-2000; 2000US-0215323P.
 XX
 PA (ELAN-) ELAN PHARM INC.
 PA (PHAA) PHARMACIA & UPJOHN CO.
 XX
 PI Beck JP, Gailunas A, Hom R, Jagodzinska B, John V, Maillaird M;
 XX
 DR WPI; 2002-122550/16.
 XX
 PT New disubstituted amine derivatives, useful for treating Alzheimer's
 PT disease and other degenerative diseases.
 XX
 PS Example D; Page 163; 286pp; English.
 XX
 CC The invention relates to disubstituted amine derivative compounds useful
 CC for treating Alzheimer's disease and other degenerative diseases.
 CC Compounds of the invention possess beta secretase inhibitory activity and
 CC are useful for inhibiting beta-secretase mediated cleavage of amyloid
 CC precursor protein (APP) and particularly, to inhibit the production of
 CC amyloid beta (A beta) peptide. They are useful for treating or preventing
 CC a disease characterised by beta-amyloid deposits in the brain e.g. for
 CC treating or preventing Alzheimer's disease (AD), for helping to prevent
 CC or delay the onset of Alzheimer's disease, for treating mild cognitive
 CC impairment (MCI), Down's syndrome, hereditary cerebral haemorrhage with
 CC the amyloidosis of the Dutch type, cerebral amyloid angiopathy and
 CC preventing its potential consequences i.e. single and recurrent lobar
 CC haemorrhages, for treating other degenerative dementias including
 CC dementias of mixed vascular and degenerative origin, dementia associated
 CC with Parkinson's disease, dementia associated with progressive
 CC supranuclear palsy, dementia associated with cortical basal degeneration
 CC and diffuse Lewy body type of Alzheimer's disease. The present sequence
 CC is oligopeptide substrate used in assay of the invention
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 8; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAEF 8
| | | | |
Db 2 EVNLDAEF 9

RESULT 15

AAU74837

ID AAU74837 standard; peptide; 9 AA.

XX

AC AAU74837;

XX

DT 09-APR-2002 (first entry)

XX

DE Synthetic amyloid precursor protein (APP) oligopeptide substrate #1.

XX

KW Amyloid precursor protein; APP; Alzheimer's disease; amine XV; nootropic;

KW neuroprotective; cerebroprotective; haemostatic; antiparkinsonian;

KW beta-secretase; amyloid beta peptide; amyloidosis; beta-amyloid plaque;

KW mild cognitive impairment; MCI; Down's syndrome;

KW hereditary cerebral haemorrhage; cortical basal degeneration;

KW cerebral amyloid angiopathy; lobar haemorrhage; degenerative dementia;

KW Parkinson's disease; supranuclear palsy; dementia.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Cleavagesite 5. .6

FT /note= "Beta-secretase cleavage site"

XX

PN WO200202506-A2.

XX

PD 10-JAN-2002.

XX

PF 29-JUN-2001; 2001WO-US020930.

XX

PR 30-JUN-2000; 2000US-0215323P.

XX

PA (ELAN-) ELAN PHARM INC.

XX

PI Fang LY, John V;

XX

DR WPI; 2002-147995/19.

XX

PT New substituted amines are e.g. amyloid beta peptide production

PT inhibitors, useful for treating or preventing e.g. Alzheimer's disease,

PT mild cognitive impairment and other degenerative diseases.

XX

PS Example D; Page 118; 434pp; English.

XX

CC This invention relates to a novel substituted amine of formula XV and its

CC salts which can be used to treat Alzheimer's disease and similar

CC diseases. The compound of the invention may have nootropic,

CC neuroprotective, cerebroprotective, haemostatic and antiparkinsonian

CC activities. The amine acts as a beta-secretase activity inhibitor,
 CC inhibiting cleavage of amyloid precursor protein (APP) and the formation
 CC of amyloid beta peptide and beta-amyloid plaque production. The amine of
 CC the invention is useful for treating or preventing a disease
 CC characterised by beta-amyloid deposits in the brain e.g. Alzheimer's
 CC disease (AD), for treating mild cognitive impairment (MCI), preventing or
 CC delaying the onset of Alzheimer's disease in those who would progress
 CC from MCI to AD, for treating Down's syndrome, humans who have hereditary
 CC cerebral haemorrhage with the Amyloidosis of the Dutch type, cerebral
 CC amyloid angiopathy and preventing its potential consequences i.e. single
 CC and recurrent lobar haemorrhages, for treating other degenerative
 CC dementias, including dementias of mixed vascular and degenerative origin,
 CC dementia associated with Parkinson's disease, dementia associated with
 CC progressive supranuclear palsy, dementia associated with cortical basal
 CC degeneration and diffuse Lewy body type of Alzheimer's disease. The
 CC present sequence represents a synthetic APP oligopeptide substrate #1 for
 CC the beta secretase enzyme. This synthetic substrate was used to test the
 CC efficiency of the amine as an inhibitor of beta secretase enzyme activity
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 8; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVNLDAEF 8
 |||||
 Db 2 EVNLDAEF 9

RESULT 16

ABB07598

ID ABB07598 standard; peptide; 9 AA.

XX

AC ABB07598;

XX

DT 08-MAY-2002 (first entry)

XX

DE Synthetic oligopeptide substrate having beta-secretase cleavage site.

XX

KW APP; amine derivative; beta-secretase; amyloid precursor protein; A beta;

KW amyloid beta peptide; beta-amyloid; nootropic; neuroprotective;

KW cerebroprotective; haemostatic; antiparkinsonian.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Cleavage-site 5. .6

FT /note= "beta-secretase cleavage site"

XX

PN WO200202520-A2.

XX

PD 10-JAN-2002.

XX

PF 02-JUL-2001; 2001WO-US021000.

XX

PR 30-JUN-2000; 2000US-0215323P.

PR 29-JUN-2001; 2001US-00895843.
 XX
 PA (ELAN-) ELAN PHARM INC.
 PA (PHAA) PHARMACIA & UPJOHN CO.
 XX
 PI Beck JP, Gailunas A, Hom R, Jagodzinska B, John V, Maillaird M;
 XX
 DR WPI; 2002-188416/24.
 XX
 PT New disubstituted amine derivatives, useful for treating Alzheimer's
 PT disease and other degenerative diseases.
 XX
 PS Example D; Page 163; 286pp; English.
 XX
 CC The invention relates to disubstituted amine derivatives of specified
 CC formulae or their salts. The amine derivatives can inhibit beta-secretase
 CC activity or inhibit the cleavage of amyloid precursor protein (APP) in a
 CC reaction mixture. They can also be used to inhibit production of amyloid
 CC beta peptide (A beta) in a cell or inhibit production of beta-amyloid
 CC plaque in an animal. The amine derivatives are useful for treating or
 CC preventing a disease characterized by beta-amyloid deposits in the brain
 CC e.g. for treating or preventing Alzheimer's disease (AD), for helping
 CC prevent or delay the onset of AD, for treating mild cognitive impairment
 CC (MCI), preventing or delaying the onset of AD in those who would progress
 CC from MCI to AD, for treating Down's syndrome, humans who have hereditary
 CC cerebral haemorrhage with the Amyloidosis of the Dutch type, cerebral
 CC amyloid angiopathy and preventing its potential consequences i.e. single
 CC and recurrent lobar haemorrhages, for treating other degenerative
 CC dementias, including dementias of mixed vascular and degenerative origin,
 CC dementia associated with Parkinson's disease, dementia associated with
 CC progressive supranuclear palsy, dementia associated with cortical basal
 CC degeneration, diffuse Lewy body type of Alzheimer's disease. Sequences
 CC ABB07598-599 are synthetic APP oligopeptide substrates containing the
 CC cleavage site of beta-secretase, used to assay beta-secretase activity
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 8; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVNLDAEF 8
 |||||
 Db 2 EVNLDAEF 9

RESULT 17
 AAM50897

ID AAM50897 standard; peptide; 9 AA.
 XX
 AC AAM50897;
 XX
 DT 07-MAY-2002 (first entry)
 XX
 DE Oligopeptide substrate for beta-secretase.
 XX
 KW Beta-secretase; substrate; amyloid precursor protein; APP;

KW amyloid beta peptide; inhibitor; screening; neurodegenerative disorder;
 KW cognitive impairment; Down's syndrome; Alzheimer's disease;
 KW hereditary cerebral haemorrhage; cerebral amyloid angiopathy; dementia;
 KW therapy.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Cleavage-site 5. .6
 XX
 PN WO200202512-A2.
 XX
 PD 10-JAN-2002.
 XX
 PF 29-JUN-2001; 2001WO-US021012.
 XX
 PR 30-JUN-2000; 2000US-0215323P.
 PR 22-NOV-2000; 2000US-0252736P.
 PR 15-DEC-2000; 2000US-0255956P.
 PR 13-FEB-2001; 2001US-0268497P.
 PR 29-MAR-2001; 2001US-0279779P.
 PR 04-JUN-2001; 2001US-0295589P.
 XX
 PA (ELAN-) ELAN PHARM INC.
 PA (PHAA) PHARMACIA & UPJOHN CO.
 XX
 PI Maillaird M, Hom C, Gailunas A, Jagodzinska B, Fang LY, John V;
 PI Freskos JN, Pulley SR, Beck JP, Tenbrink RE;
 XX
 DR WPI; 2002-171627/22.
 XX
 PT New substituted amines are e.g. amyloid beta peptide production
 PT inhibitors, useful for treating or preventing e.g. Alzheimer's disease,
 PT mild cognitive impairment and other degenerative diseases.
 XX
 PS Example D; Page 344; 65lpp; English.
 XX
 CC The present sequence is that of a peptide that incorporates the known
 CC cleavage site of beta-secretase on amyloid precursor protein (APP). The
 CC peptide, which may optionally be tagged with a fluorescent or chromogenic
 CC moiety, can be used in assays to determine the beta-secretase inhibitory
 CC activity of novel substituted amine compounds of the invention.
 CC Comparison of substrate cleavage results in the presence of an inhibitor
 CC and in the presence of a control provides a measure of the compound's
 CC inhibitory activity. Novel compounds of the invention are effective
 CC inhibitors of beta-secretase, inhibit beta-secretase mediated cleavage of
 CC APP, are effective inhibitors of A beta production, and/or effectively
 CC reduce amyloid beta deposits or plaques. They are used in the treatment
 CC or prevention of diseases characterised by amyloid deposits in the brain,
 CC e.g. for treating or preventing Alzheimer's disease (AD), for helping
 CC prevent or delay the onset of AD, for treating mild cognitive impairment
 CC (MCI), preventing or delaying the onset of AD in those who would progress
 CC from MCI to AD, for treating Down's syndrome and hereditary cerebral
 CC haemorrhage with Amyloidosis of the Dutch type, for treating cerebral
 CC amyloid angiopathy and preventing its potential consequences i.e. single
 CC and recurrent lobar haemorrhages, for treating other degenerative
 CC dementias, including dementias of mixed vascular and degenerative origin,

CC dementia associated with Parkinson's disease, dementia associated with
CC progressive supranuclear palsy, and dementia associated with cortical
CC basal degeneration, and for treating diffuse Lewy body type of AD (all
CC claimed)

XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 8; DB 5; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.4e+06;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAEF 8

|||||||

Db 2 EVNLDAEF 9

RESULT 18

ABP97975

ID ABP97975 standard; peptide; 9 AA.

XX

AC ABP97975;

XX

DT 17-JUN-2003 (first entry)

XX

DE Synthetic substrate comprising beta-secretase cleavage site.

XX

KW Substrate; beta-secretase; alkylamide derivative; Alzheimer's disease;

KW cognitive impairment; Down's syndrome; Hereditary Cerebral Haemorrhage;

KW Parkinson's disease; cerebral amyloid angiopathy; degenerative dementia;

KW supranuclear palsy; cortical basal degeneration.

XX

OS Synthetic.

XX

PN WO2003006423-A1.

XX

PD 23-JAN-2003.

XX

PF 11-JUL-2002; 2002WO-US022255.

XX

PR 11-JUL-2001; 2001US-0304525P.

PR 30-JUL-2001; 2001US-0308756P.

PR 17-DEC-2001; 2001US-0341341P.

PR 17-DEC-2001; 2001US-0341416P.

PR 21-DEC-2001; 2001US-0344872P.

PR 21-DEC-2001; 2001US-0380574P.

XX

PA (ELAN-) ELAN PHARM INC.

PA (PHAA) PHARMACIA & UPJOHN CO.

XX

PI Gailunas A, Hom R, John V, Maillard M, Chrusciel RA, Fisher J;

PI Jacobs J, Freskos JN, Brown DL, Fobian YM;

XX

DR WPI; 2003-239223/23.

XX

PT New N-(3-amino-2-hydroxypropyl) alkylamide derivatives are beta secretase

PT inhibitors used for treating e.g. Alzheimer's disease and Down's

PT syndrome.

XX
PS Example D; Page 139; 205pp; English.

XX
CC The present sequence represents a synthetic substrate comprising a beta-secretase cleavage site. The substrate was used to assay beta-secretase activity in the presence or absence of inhibitory compounds of the invention. The invention describes N-(3-Amino-2-hydroxypropyl) alkylamide derivatives of a formula given in the specification. Compounds of the invention are used for treating or preventing Alzheimer's disease, mild cognitive impairment, Down's syndrome, Hereditary Cerebral Haemorrhage with Amyloidosis of the Dutch-Type, cerebral amyloid angiopathy, other degenerative dementias and diffuse Lewy body type of Alzheimer's disease. They are also used for dementias of mixed vascular and degenerative origin, dementia associated with Parkinson's disease, dementia associated with progressive supranuclear palsy and dementia associated with cortical basal degeneration

XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 8; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAEF 8
| | | | | | | |
Db 2 EVNLDAEF 9

RESULT 19

ABP57515

ID ABP57515 standard; peptide; 9 AA.

XX

AC ABP57515;

XX

DT 28-APR-2003 (first entry)

XX

DE Differentially isotopically labelled (DiMaS) peptide #8.

XX

KW Mass spectrometry; polymer; analysis; cleavage; substrate specificity;
KW isotope; protease.

XX

OS Synthetic.

XX

PN WO2003001206-A1.

XX

PD 03-JAN-2003.

XX

PF 25-JUN-2002; 2002WO-GB002921.

XX

PR 26-JUN-2001; 2001GB-00015581.

XX

PA (GLAX) GLAXO GROUP LTD.

XX

PI Mckeown SC;

XX

DR WPI; 2003-184066/18.

XX

PT Analyzing cleavage of polymer, by providing polymer sample, incubating
PT the sample with labeled isotope for cleavage at potential cleavage site,
PT and analyzing the masses of any uncleaved fragments by mass spectrometry.

XX

PS Example 3; Page 25; 73pp; English.

XX

CC The present invention describes a method (M1) for analysing cleavage of a
CC polymer. M1 comprises: (a) providing a sample of the polymer, a portion
CC of the polymer molecules having been labeled at a position on one side of
CC the potential cleavage site with a first isotopic label and a portion of
CC the polymer molecules having been labeled at a position on the opposite
CC side of the potential cleavage site with a second isotopic label; (b)
CC incubating the sample under conditions suitable for cleavage at the
CC potential cleavage site; and (c) analysing the mass(es) of any cleaved
CC fragments by mass spectrometry and thereby determining whether and/or
CC where cleavage has taken place. M1 is useful for analysing cleavage of a
CC polymer, where the polymer is a linear polymer, and comprises a peptide
CC or protein. Methods from the present invention can be used in discovering
CC new or improved synthetic substrates for both known and unknown enzymes,
CC e.g. enzymes identified from the human genome. The methods are also
CC useful to identify the sequence origin, and in screening methods to
CC identify new substrates for enzymes, in positional peptide scanning
CC libraries, in in vivo/ex vivo/in vitro peptide, and in assaying methods
CC for oligonucleotide or peptide sequencing and in measuring differential
CC protein expression. The methods are useful for monitoring the cleavage of
CC polypeptides or polynucleotides, and for determining optimal polymer
CC substrates. ABP57505 to ABP57605 represent peptides used in the
CC exemplification of the present invention

XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 8; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVNLDAEF 8

|||||||

Db 2 EVNLDAEF 9

RESULT 20

ABP57084

ID ABP57084 standard; peptide; 9 AA.

XX

AC ABP57084;

XX

DT 14-APR-2003 (first entry)

XX

DE Synthetic oligopeptide substrate SEQ ID NO:8.

XX

KW Beta-hydroxyamine derivative; nootropic; neuroprotective; MCI;

KW Alzheimer's disease; mild cognitive impairment; Down's syndrome;

KW hereditary cerebral haemorrhage; amyloidosis; lobar haemorrhage;

KW cerebral amyloid angiopathy; degenerative dementia; dementia;

KW Parkinson's disease; progressive supranuclear palsy; APP;

KW cortical basal degeneration; amyloid precursor protein; substrate.

XX

```

OS   Synthetic.
XX
FH   Key                      Location/Qualifiers
FT   Modified-site           1
FT                                   /note= "biotinylated"
XX
PN   WO2003002122-A1.
XX
PD   09-JAN-2003.
XX
PF   27-JUN-2002; 2002WO-US020754.
XX
PR   27-JUN-2001; 2001US-0301210P.
PR   18-SEP-2001; 2001US-0323396P.
PR   19-NOV-2001; 2001US-0332736P.
XX
PA   (ELAN-) ELAN PHARM INC.
PA   (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI   John V,  Hom R,  Tucker J;
XX
DR   WPI; 2003-201464/19.
XX
PT   New beta-hydroxyamine derivatives are beta secretase inhibitors used for
PT   treating e.g. Alzheimer's disease, Down's syndrome and cerebral amyloid
PT   angiopathy.
XX
PS   Example D; Page 56; 96pp; English.
XX
CC   The present invention describes beta-hydroxyamine derivatives (I). Also
CC   described is a method for the preparation of (I). (I) has nootropic and
CC   neuroprotective activities. (I) can be used as an inhibitor of: beta-
CC   secretase activity; beta amyloid peptide (A beta) production; beta
CC   deposition; and amyloid precursor protein (APP) cleavage. (I) can be used
CC   for preventing or delaying the onset of Alzheimer's disease, for treating
CC   mild cognitive impairment (MCI), Down's syndrome, hereditary cerebral
CC   haemorrhage with amyloidosis of the Dutch-type and cerebral amyloid
CC   angiopathy and preventing its potential consequences i.e. single and
CC   recurrent lobar haemorrhages, for treating other degenerative dementias
CC   (including dementias of mixed vascular and degenerative origin, dementia
CC   associated with Parkinson's disease, dementia associated with progressive
CC   supranuclear palsy, dementia associated with cortical basal degeneration)
CC   or diffuse Lewy body type of Alzheimer's disease. The present sequence
CC   represents a synthetic oligopeptide substrate, which is used in the
CC   exemplification of the present invention
XX
SQ   Sequence 9 AA;

Query Match          100.0%;  Score 8;  DB 6;  Length 9;
Best Local Similarity 100.0%;  Pred. No. 1.4e+06;
Matches      8;  Conservative    0;  Mismatches    0;  Indels      0;  Gaps      0;

QY          1 EVNLDAEF 8
              |||||
Db          2 EVNLDAEF 9

```

RESULT 21

ABP71468

ID ABP71468 standard; peptide; 9 AA.

XX

AC ABP71468;

XX

DT 15-MAY-2003 (first entry)

XX

DE Beta-secretase cleavage site comprising oligopeptide.

XX

KW APP; alpha-hydroxyamide statine; nootropic; neuroprotective; haemostatic;

KW beta-secretase; beta Amyloid; A beta; amyloid precursor protein;

KW degenerative dementia; Alzheimer's disease; Down's syndrome;

KW Hereditary Cerebral Haemorrhage with Amyloidosis of the Dutch-Type;

KW cerebral amyloid angiopathy.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Cleavage-site 5. .6

FT /note= "beta-secretase cleavage site"

XX

PN WO2003006021-A1.

XX

PD 23-JAN-2003.

XX

PF 10-JUL-2002; 2002WO-US021742.

XX

PR 10-JUL-2001; 2001US-0304128P.

PR 05-OCT-2001; 2001US-0327424P.

XX

PA (ELAN-) ELAN PHARM INC.

PA (PHAA) PHARMACIA & UPJOHN CO.

PA (SCHO/) SCHOSTAREZ H J.

PA (CHRU/) CHRUSCIEL R A.

XX

PI Schostarez HJ, Chrusciel RA;

XX

DR WPI; 2003-267942/26.

XX

PT New alpha-hydroxyamide statine derivatives useful for the treatment of
PT e.g. Alzheimer's disease.

XX

PS Example D; Page 97; 142pp; English.

XX

CC The invention relates to alpha-hydroxyamide statine derivatives of
CC specified formula. The compounds are capable of slowing beta amyloid
CC peptide (A beta) formation and/or deposition in the brain and are
CC effective inhibitors of beta-secretase. They inhibit beta-secretase-
CC mediated cleavage of APP and are effective inhibitors of A beta
CC production to reduce amyloid beta deposit or plaques. The compounds are
CC useful in the manufacture of a medicament for treating or preventing e.g.
CC Alzheimer's disease, mild cognitive impairment, Down's syndrome,
CC Hereditary Cerebral Haemorrhage with Amyloidosis of the Dutch-Type,
CC cerebral amyloid angiopathy, other degenerative dementias (including
CC dementias of mixed vascular and degenerative origin, dementia associated
CC with Parkinson's disease, dementia associated with progressive

CC supranuclear palsy, dementia associated with cortical basal degeneration)
CC or diffuse Lewy body type of Alzheimer's disease in a patient. The
CC present sequence represents an oligopeptide that incorporates the known
CC beta-secretase cleavage site, used in assays for beta-secretase
CC inhibition by the inhibitory compounds of the invention
XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 8; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVNLDAEF 8
|||
Db 2 EVNLDAEF 9

RESULT 22

AAO16449

ID AAO16449 standard; peptide; 9 AA.

XX

AC AAO16449;

XX

DT 10-APR-2003 (first entry)

XX

DE Beta-secretase synthetic APP substrate peptide, SEQ ID No 8.

XX

KW Alzheimer's disease; bicyclo compound; amyloid beta peptide;

KW beta-amyloid plaque; cognitive activity; amyloid precursor protein; APP;

KW degenerative dementia; Parkinson's disease; cerebral amyloid angiopathy;

KW beta-secretase; substrate.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "Labelled with biotin"

FT Cleavage-site 5. .6

FT /note= "Cleaved between these two residues by beta-secretase"

XX

PN WO2003000261-A1.

XX

PD 03-JAN-2003.

XX

PF 25-JUN-2002; 2002WO-US020054.

XX

PR 25-JUN-2001; 2001US-0300671P.

XX

PA (ELAN-) ELAN PHARM INC.

PA (PHAA) PHARMACIA & UPJOHN CO.

XX

PI Beck JP;

XX

DR WPI; 2003-201375/19.

XX

PT Treatment or prevention of Alzheimer's disease involves use of bicyclo

PT compounds.
 XX
 PS Example D; Page 60; 116pp; English.
 XX
 CC The invention comprises a method for the treatment or prevention of
 CC Alzheimer's disease. The method involves the administration of bicyclo
 CC compounds or their salts. A major factor in the development of
 CC Alzheimer's disease is the deposition of amyloid beta peptide (beta-
 CC amyloid plaques) in areas of the brain responsible for cognitive
 CC activities. Amyloid beta protein is derived by proteolysis (by
 CC secretases) of the amyloid precursor protein (APP). The method of the
 CC invention is useful for treating and delaying the onset of Alzheimer's
 CC disease. The method is also useful for the treatment of other
 CC degenerative dementias (e.g. Parkinson's disease and cerebral amyloid
 CC angiopathy). The method of the invention is useful for inhibiting beta-
 CC secretase activity - thereby inhibiting cleavage of an APP and inhibiting
 CC production of amyloid beta peptide. The present amino acid sequence
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 8; DB 6; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVNLDAEF 8
 |||||
 Db 2 EVNLDAEF 9

RESULT 23

ABP71269

ID ABP71269 standard; peptide; 9 AA.

XX

AC ABP71269;

XX

DT 28-APR-2003 (first entry)

XX

DE Oligopeptide substrate used for beta-secretase assay.

XX

KW APP; aminediol; amyloid precursor protein; beta amyloid; A-beta;

KW beta-secretase; nootropic; neuroprotective; antiparkinsonian;

KW cerebroprotective; haemostatic.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "N-terminal biotinylation"

FT Cleavage-site 5. .6

FT /note= "cleavage site for beta-secretase"

XX

PN WO2003006453-A1.

XX

PD 23-JAN-2003.

XX

PF 10-JUL-2002; 2002WO-US021709.

XX
 PR 10-JUL-2001; 2001US-0304129P.
 XX
 PA (ELAN-) ELAN PHARM INC.
 PA (PHAA) PHARMACIA & UPJOHN CO.
 XX
 PI Schostarez HJ, Chrusciel RA;
 XX
 DR WPI; 2003-210414/20.
 XX
 PT New aminediols are beta-secretase inhibitors, useful for the treatment of
 PT e.g. Alzheimer's disease, cognitive impairment, Down's syndrome, and
 PT degenerative dementias.
 XX
 PS Example D; Page 145; 190pp; English.
 XX
 CC The invention relates to aminediol derivatives of specified formula. The
 CC compounds are capable of slowing beta amyloid (A-beta) peptide formation
 CC and/or deposition in the brain. They are effective inhibitors of beta-
 CC secretase and inhibit beta-secretase-mediated cleavage of amyloid
 CC precursor protein (APP). Thus they effectively inhibit A-beta production
 CC and helps to reduce amyloid beta deposit or plaques. The compounds are
 CC useful in the manufacture of a medicament for treating or preventing
 CC Alzheimer's disease, mild cognitive impairment, Down's syndrome,
 CC Hereditary Cerebral Haemorrhage with Amyloidosis of the Dutch-Type,
 CC cerebral amyloid angiopathy, other degenerative dementias (including
 CC dementias of mixed vascular and degenerative origin, dementia associated
 CC with Parkinson's disease, dementia associated with progressive
 CC supranuclear palsy, dementia associated with cortical basal degeneration)
 CC or diffuse Lewy body type of Alzheimer's disease in a patient especially
 CC human. Sequences ABP71269-270 represent oligopeptide substrates
 CC containing known beta-secretase cleavage site are used to assay beta-
 CC secretase activity
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 8; DB 6; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAEF 8
 |||||
 Db 2 EVNLDAEF 9

RESULT 24

ABR44377

ID ABR44377 standard; peptide; 9 AA.

XX

AC ABR44377;

XX

DT 14-JUL-2003 (first entry)

XX

DE Oligonpeptide #1 incorporating cleavage site of beta-secretase.

XX

KW Nootropic; neuroprotective; hemostatic; Alzheimer's disease;

KW Down's syndrome; Hereditary Cerebral Hemorrhage; beta-secretase.

XX
 OS Synthetic.
 XX
 PN WO2003027068-A2.
 XX
 PD 03-APR-2003.
 XX
 PF 24-SEP-2002; 2002WO-US030231.
 XX
 PR 24-SEP-2001; 2001US-0324407P.
 XX
 PA (ELAN-) ELAN PHARM INC.
 XX
 PI Gailunas A, Tucker JA, John V;
 XX
 DR WPI; 2003-421148/39.
 XX
 PT New substituted amines useful for the treatment of e.g. Alzheimer's
 PT disease, mild cognitive impairment and down's syndrome.
 XX
 PS Example D; Page 106; 140pp; English.
 XX
 CC This invention relates to substituted amines that are considered
 CC nootropic, neuroprotective and hemostatic in their action. They are
 CC useful in the manufacture of a medicament for treating or preventing
 CC Alzheimer's disease, mild cognitive impairment, Down's syndrome,
 CC Hereditary Cerebral Hemorrhage with Amyloidosis of the Dutch-Type and
 CC other degenerative dementias. The compounds are capable of slowing A-beta
 CC peptide formation and deposition in the brain and are effective
 CC inhibitors of beta-secretase that inhibit beta-secretase-mediated
 CC cleavage of APP that are effective inhibitors of A beta production and
 CC effective to reduce amyloid beta deposit or plaques. The present sequence
 CC represents a synthetic oligopeptide that incorporates the cleavage site of
 CC beta-secretase
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 8; DB 6; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVNLDAEF 8
 |||||
 Db 2 EVNLDAEF 9

RESULT 25

ABP58375

ID ABP58375 standard; peptide; 9 AA.
 XX
 AC ABP58375;
 XX
 DT 07-APR-2003 (first entry)
 XX
 DE Beta-secretase amyloid precursor protein substrate.
 XX
 KW Beta-secretase; substrate; amyloid precursor protein; inhibitor;

KW hydroxyl alkyl amine; Alzheimer's disease; nootropic; neuroprotective;
 KW haemostatic; antiparkinsonian.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Cleavage-site 5. .6
 XX
 PN WO200298849-A2.
 XX
 PD 12-DEC-2002.
 XX
 PF 31-MAY-2002; 2002WO-US017698.
 XX
 PR 01-JUN-2001; 2001US-0295332P.
 PR 19-NOV-2001; 2001US-0332639P.
 PR 28-DEC-2001; 2001US-0343772P.
 XX
 PA (ELAN-) ELAN PHARM INC.
 PA (PHAA) PHARMACIA & UPJOHN CO.
 XX
 PI Freskos J, Aquino J, Brown DL, Fang L, Fobian YM, Gailunas A;
 PI Guinn A, Varghese J, Romero AG, Tucker J, Tung J, Walker D;
 XX
 DR WPI; 2003-201287/19.
 XX
 PT New hydroxy alkyl amine compounds are beta-secretase activity inhibitors
 PT useful for treatment of e.g. Alzheimer's disease, mild cognitive
 PT impairment, Down's syndrome, hereditary cerebral hemorrhage.
 XX
 PS Example D; Page 197; 360pp; English.
 XX
 CC The present sequence is an example of a synthetic amyloid precursor
 CC protein (APP) substrate that includes a beta-secretase cleavage site.
 CC Cleavage products can be detected using HPLC, or fluorogenic or
 CC chromogenic detection methods. The invention provides novel hydroxy alkyl
 CC amine compounds that have beta-secretase inhibitor activity. Beta-
 CC secretase cleaves APP to amyloid beta peptide, found in the brains of
 CC Alzheimer's disease patients. The novel compounds halt or reduce A-beta
 CC production from APP and reduce or eliminate the formation of beta-amyloid
 CC deposits in the brain. They are useful for the manufacture of a
 CC medicament for the treatment or prevention of Alzheimer's disease, mild
 CC cognitive impairment, Down's syndrome, hereditary cerebral haemorrhage
 CC with amyloidosis of the Dutch type, cerebral amyloid angiopathy, other
 CC degenerative dementias, dementias of mixed vascular and degenerative
 CC origin, dementia associated with Parkinson's disease, dementia associated
 CC with progressive supranuclear palsy, dementia associated with cortical
 CC basal degeneration, diffuse Lewy body type of Alzheimer's disease (all
 CC claimed) and for treating frontotemporal dementias with parkinsonism
 XX
 SQ Sequence 9 AA;

 Query Match 100.0%; Score 8; DB 6; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 EVNLDAEF 8

Db

|||||||
2 EVNLDAEF 9

RESULT 26

AAO26801

ID AAO26801 standard; peptide; 9 AA.

XX

AC AAO26801;

XX

DT 10-APR-2003 (first entry)

XX

DE Beta-secretase substrate peptide, SEQ ID No 8.

XX

KW Nootropic; neuroprotective; haemostatic; antiparkinsonian; aminoalcohol;

KW Alzheimer's disease; mild cognitive impairment; MCI; Down's syndrome;

KW Hereditary Cerebral Haemorrhage; Amyloidosis; Dutch-Type;

KW cerebral amyloid angiopathy; single; recurrent lobar haemorrhages;

KW degenerative dementia; Parkinson's disease; cortical basal degeneration;

KW progressive supranuclear palsy; Lewy body type; beta-secretase; enzyme;
substrate.

XX

OS Unidentified.

XX

PN WO2002100820-A1.

XX

PD 19-DEC-2002.

XX

PF 11-JUN-2002; 2002WO-US019067.

XX

PR 11-JUN-2001; 2001US-0297420P.

XX

PA (ELAN-) ELAN PHARM INC.

PA (PHAA) PHARMACIA & UPJOHN CO.

XX

PI Maillard M, Tucker JA;

XX

DR WPI; 2003-167387/16.

XX

PT New substituted aminoalcohols useful for the treatment of e.g.

PT Alzheimer's disease, mild cognitive impairment, Down's syndrome or

PT dementia associated with Parkinson's disease.

XX

PS Example D; Page 119; 206pp; English.

XX

CC The invention relates to novel substituted aminoalcohols, their esters
CC and salts. The novel substituted aminoalcohols can be used for treating a
CC patient who has, or in preventing a patient from getting, a disease or
CC condition (e.g. Alzheimer's disease), for helping prevent or delay the
CC onset of the Alzheimer's disease, for treating patients with mild
CC cognitive impairment (MCI) and preventing or delaying the onset of
CC Alzheimer's disease in those who would progress from MCI to Alzheimer's
CC disease, for treating Down's syndrome, for treating humans who have
CC Hereditary Cerebral Haemorrhage with Amyloidosis of the Dutch-Type, for
CC treating cerebral amyloid angiopathy and preventing its potential
CC consequences i.e. single and recurrent lobar haemorrhages, for treating
CC other degenerative dementias (including dementias of mixed vascular and

CC degenerative origin, dementia associated with Parkinson's disease,
CC dementia associated with progressive supranuclear palsy, dementia
CC associated with cortical basal degeneration) or diffuse Lewy body type of
CC Alzheimer's disease. This sequence represents a peptide substrate of beta
CC -secretase used in an enzyme inhibition assay for analysing the
CC inhibitory activity of the novel compounds of the invention
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 8; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAEF 8
 |||||||
Db 2 EVNLDAEF 9

RESULT 27

ABG75940

ID ABG75940 standard; peptide; 9 AA.

XX

AC ABG75940;

XX

DT 07-MAY-2003 (first entry)

XX

DE Synthetic Amyloid precursor protein (APP) substrate #6.

XX

KW Amyloid precursor protein; APP; substituted cyclic amide;

KW Alzheimer's disease; mild cognitive impairment; MCI; Down's syndrome;

KW hereditary cerebral haemorrhage with Amyloidosis of the dutch type;

KW cerebral amyloid angiopathy; degenerative dementia; dementia;

KW diffuse Lewy body type of Alzheimer's disease; Parkinson's disease;

KW progressive supernuclear palsy; cortical basal degeneration;

KW beta-secretase inhibitor.

XX

OS Synthetic.

XX

PN WO2002100856-A1.

XX

PD 19-DEC-2002.

XX

PF 12-JUN-2002; 2002WO-US019076.

XX

PR 12-JUN-2001; 2001US-0297546P.

PR 19-NOV-2001; 2001US-0333083P.

XX

PA (ELAN-) ELAN PHARM INC.

PA (PHAA) PHARMACIA & UPJOHN CO.

XX

PI Pulley SR, Beck JP, Tenbrink RE;

XX

DR WPI; 2003-278223/27.

XX

PT New substituted cyclic amides useful as beta-secretase and amyloid

PT precursor protein inhibitors for treating e.g. Alzheimer's disease and

PT Down's syndrome.

XX
 PS Example D; Page 113; 164pp; English.
 XX
 CC The invention describes substituted cyclic amides (I). (I) are useful in
 CC the manufacture of a medicament for treating, preventing and delaying
 CC Alzheimer's disease, for treating mild cognitive impairment (MCI), Down's
 CC syndrome, hereditary cerebral haemorrhage with Amyloidosis of the dutch
 CC type, cerebral amyloid angiopathy, other degenerative dementias and
 CC diffuse Lewy body type of Alzheimer's disease. (I) is also useful for
 CC treating dementia associated with Parkinson's disease, progressive
 CC supernuclear palsy and cortical basal degeneration. The compounds are
 CC capable of slowing A-beta peptide formation and/or deposition in the
 CC brain and are effective inhibitors of beta-secretase, that inhibit beta-
 CC secretase-mediated cleavage of APP, that are effective inhibitors of A
 CC beta production and/or effective to reduce amyloid beta deposit or
 CC plaques. This is the amino acid sequence of an amyloid precursor protein
 CC (APP) substrate that can be cleaved by beta-secretase and is therefore
 CC used to assay beta-secretase activity in the presence and absence of the
 CC inhibitory compounds of the invention
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 8; DB 6; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAEF 8
 |||||
 Db 2 EVNLDAEF 9

RESULT 28

ABP71630

ID ABP71630 standard; peptide; 9 AA.

XX

AC ABP71630;

XX

DT 29-MAY-2003 (first entry)

XX

DE Beta-secretase activity assaying oligopeptide substrate.

XX

KW APP; diaminediol; A-beta; beta-secretase; amyloid precursor protein;
 KW beta amyloid; nootropic; neuroprotective; antiparkinsonian; haemostatic.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "N-terminal biotin"

FT Cleavage-site 5. .6

FT /note= "beta-secretase cleavage site"

XX

PN WO2003006013-A1.

XX

PD 23-JAN-2003.

XX

PF 10-JUL-2002; 2002WO-US022459.

XX
 PR 10-JUL-2001; 2001US-0304305P.
 PR 30-NOV-2001; 2001US-0334480P.
 XX
 PA (ELAN-) ELAN PHARM INC.
 PA (PHAA) PHARMACIA & UPJOHN CO.
 XX
 PI Schostarez HJ, Chrusciel RA;
 XX
 DR WPI; 2003-289727/28.
 XX
 PT New diaminediols useful for the treatment of e.g. Alzheimer's disease.
 XX
 PS Example D; Page 139; 182pp; English.
 XX
 CC The invention relates to diaminediol derivatives of specified formula.
 CC The compounds are capable of slowing A-beta peptide formation and/or
 CC deposition in the brain and are effective inhibitors of beta-secretase.
 CC They can inhibit beta-secretase-mediated cleavage of APP (amyloid
 CC precursor protein) and are effective inhibitors of A beta production and/
 CC or effective to reduce amyloid beta deposit or plaques. The compounds are
 CC useful in the manufacture of a medicament for treating or preventing e.g.
 CC Alzheimer's disease, mild cognitive impairment, Down's syndrome,
 CC Hereditary Cerebral Hemorrhage with Amyloidosis of the Dutch-Type,
 CC cerebral amyloid angiopathy, other degenerative dementias (including
 CC dementias of mixed vascular and degenerative origin, dementia associated
 CC with Parkinson's disease, dementia associated with progressive
 CC supranuclear palsy, dementia associated with cortical basal degeneration)
 CC or diffuse Lewy body type of Alzheimer's disease in a patient e.g. human.
 CC Sequences ABP71630-631 represent synthetic APP oligopeptide substrates
 CC containing the known beta-secretase cleavage site and are used to assay
 CC beta-secretase activity
 XX
 SQ Sequence 9 AA;

 Query Match 100.0%; Score 8; DB 6; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 EVNLDAEF 8
 |||||
 Db 2 EVNLDAEF 9

 RESULT 29
 AAE36000
 ID AAE36000 standard; peptide; 9 AA.
 XX
 AC AAE36000;
 XX
 DT 26-JUN-2003 (first entry)
 XX
 DE APP substrate #6 used in the exemplification of the invention.
 XX
 KW Aminatediol compound; beta secretase inhibitor; Alzheimer's disease; AD;
 KW Hereditary Cerebral Haemorrhage with Amyloidosis of Dutch-Type; HCHWA-D;
 KW cognitive impairment; cerebral amyloid angiopathy; Down's syndrome; APP;

KW amyloidosis; cortical basal degeneration; Parkinson's disease; therapy;
KW dementia; supranuclear palsy; amyloid precursor protein.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Cleavage-site 5. .6
XX
PN WO2002100818-A2.
XX
PD 19-DEC-2002.
XX
PF 13-JUN-2002; 2002WO-US018845.
XX
PR 13-JUN-2001; 2001US-0297827P.
PR 19-NOV-2001; 2001US-0333084P.
XX
PA (ELAN-) ELAN PHARM INC.
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Schostarez HJ, Chrusciel RA;
XX
DR WPI; 2003-201321/19.
XX
PT New aminediol compounds are beta secretase inhibitors used for treating
PT e.g. Alzheimer's disease and dementia associated with Alzheimer's
PT disease.
XX
PS Example C; Page 160; 213pp; English.
XX
CC The invention relates to aminediol compounds including beta secretase
CC inhibitors, used for treating and preventing Alzheimer's disease (AD),
CC mild cognitive impairment, Down's syndrome, Hereditary Cerebral
CC Haemorrhage with Amyloidosis of Dutch-Type (HCHWA-D), cerebral amyloid
CC angiopathy, other degenerative dementias, dementias of mixed vascular and
CC degenerative origin, dementia associated with Parkinson's disease,
CC dementia associated with progressive supranuclear palsy, dementia
CC associated with cortical basal degeneration and diffuse Lewy body type of
CC Alzheimer's disease. The present sequence is APP (amyloid precursor
CC protein) substrate used in the exemplification of the invention
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 8; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAEF 8
| | | | | | | |
Db 2 EVNLDAEF 9

RESULT 30
ABR82372
ID ABR82372 standard; peptide; 9 AA.
XX
AC ABR82372;

XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Beta-secretase cleavage site containing oligopeptide substrate.
 XX
 KW APP; amino carboxamide; nootropic; neuroprotective; haemostatic;
 KW antiparkinsonian; beta-secretase; amyloid precursor protein.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "N-terminal biotinylation"
 FT Cleavage-site 5. .6
 FT /note= "beta-secretase cleavage site"
 XX
 PN WO2003057721-A2.
 XX
 PD 17-JUL-2003.
 XX
 PF 06-JAN-2003; 2003WO-US000326.
 XX
 PR 04-JAN-2002; 2002US-0345316P.
 PR 18-JAN-2002; 2002US-0350419P.
 XX
 PA (ELAN-) ELAN PHARM INC.
 PA (PHAA) PHARMACIA & UPJOHN CO.
 XX
 PI Jagodzinska B, Warpehoski MA;
 XX
 DR WPI; 2003-645986/61.
 XX
 PT New substituted amino carboxamide compounds are beta secretase inhibitors
 PT used for treating e.g. Alzheimer's disease and mild cognitive impairment
 PT and Down's syndrome.
 XX
 PS Example D; Page 101; 133pp; English.
 XX
 CC The invention relates to substituted amino carboxamide compounds of
 CC specified formula. The compounds can inhibit the activity beta-secretase
 CC and can also inhibit amyloid precursor protein (APP) cleavage. They can
 CC be used for treatment or prevention of Alzheimer's disease, mild
 CC cognitive impairment, Down's syndrome, hereditary cerebral haemorrhage
 CC with amyloidosis of the Dutch-type, cerebral amyloid angiopathy, other
 CC degenerative dementias, dementias of mixed vascular and degenerative
 CC origin, dementia associated with Parkinson's disease, dementia associated
 CC with progressive supranuclear palsy, dementia associated with cortical
 CC basal degeneration, or diffuse Lewy body type of Alzheimer's disease. The
 CC present sequence represents a synthetic oligopeptide substrate containing
 CC the known cleavage site of beta-secretase cleavage site
 XX
 SQ Sequence 9 AA;

 Query Match 100.0%; Score 8; DB 6; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAEF 8
 | | | | |
Db 2 EVNLDAEF 9

RESULT 31

ABR56258

ID ABR56258 standard; peptide; 9 AA.

XX

AC ABR56258;

XX

DT 20-NOV-2003 (first entry)

XX

DE Amyloid Precursor Protein substrate #6.

XX

KW APP; nootropic; neuroprotective; cerebroprotective; Alzheimer's disease;

KW beta-secretase; Amyloid Precursor Protein.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "Biotin-Ser"

FT Cleavage-site 5. .6

XX

PN WO2003043618-A2.

XX

PD 30-MAY-2003.

XX

PF 19-NOV-2002; 2002WO-US037180.

XX

PR 19-NOV-2001; 2001US-0332863P.

XX

PA (ELAN-) ELAN PHARM INC.

PA (PHAA) PHARMACIA & UPJOHN.

XX

PI Schostarez HJ, Hanson GJ;

XX

DR WPI; 2003-532662/50.

XX

PT Treatment of Alzheimer's disease involves the use of amine diols or their salts.

XX

PS Example D; Page 227; 270pp; English.

XX

CC The present invention relates to novel amine diols and their salts, which
CC can be used for the treatment of Alzheimer's disease. The compounds are
CC inhibitors of beta-secretase, which cleaves Amyloid Precursor Protein
CC (APP) to produce A beta peptide, a major component of the amyloid plaques
CC found in the brains of Alzheimer's sufferers. APP substrates (ABR56251-
CC ABR56259) that can be cleaved by beta-secretase, were used to assay beta-
CC secretase activity in the presence or absence of the compounds of the
CC invention

XX

SQ Sequence 9 AA;

Query Match

100.0%; Score 8; DB 6; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAEF 8
| | | | | | | |
Db 2 EVNLDAEF 9

RESULT 32

ABR62018

ID ABR62018 standard; peptide; 9 AA.

XX

AC ABR62018;

XX

DT 03-OCT-2003 (first entry)

XX

DE Beta-secretase cleavage site containing oligopeptide substrate.

XX

KW APP; Alzheimer's disease; nootropic; neuroprotective; cerebroprotective;
KW beta amyloid peptide; amyloid precursor protein; beta-secretase; A beta;
KW haemostatic.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "N-terminal biotinylation"

FT Cleavage-site 5. .6

XX

PN WO2003047576-A1.

XX

PD 12-JUN-2003.

XX

PF 03-DEC-2002; 2002WO-US040038.

XX

PR 04-DEC-2001; 2001US-0336566P.

XX

PA (ELAN-) ELAN PHARM INC.

XX

PI Varghese J;

XX

DR WPI; 2003-558913/52.

XX

PT Treating Alzheimer's disease, mild cognitive impairment and other similar
PT diseases comprises administering beta secretase inhibiting heterocyclic
PT compounds.

XX

PS Example D; Page 65; 149pp; English.

XX

CC The invention relates to treating or preventing Alzheimer's disease and
CC related diseases and involves administering heterocyclic compounds of
CC specified formula. The compounds can inhibit the activity of beta-
CC secretase. It can also inhibit the production and/or deposition of beta
CC amyloid peptide (A beta) in the brain and inhibit beta-secretase mediated
CC cleavage of amyloid precursor protein (APP). The compounds can be used
CC for treating, preventing or delaying the onset of Alzheimer's disease,
CC for treating mild cognitive impairment (MCI) and preventing or delaying

CC the onset of Alzheimer's disease in those with MCI, for treating Down's
 CC syndrome, hereditary cerebral haemorrhage with amyloidosis of the Dutch-
 CC type, cerebral amyloid angiopathy and preventing its potential
 CC consequences i.e. single and recurrent lobar haemorrhages, other
 CC degenerative dementias (including dementias of mixed vascular and
 CC degenerative origin, dementia associated with Parkinson's disease,
 CC dementia associated with progressive supranuclear palsy, dementia
 CC associated with cortical basal degeneration) or diffuse Lewy body type of
 CC Alzheimer's disease. The present sequence represents a synthetic
 CC oligopeptide substrate containing the known cleavage site of beta-
 CC secretase, used to assay beta-secretase activity
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 8; DB 6; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVNLDAEF 8
 |||||
 Db 2 EVNLDAEF 9

RESULT 33

ABR61887

ID ABR61887 standard; peptide; 9 AA.

XX

AC ABR61887;

XX

DT 12-SEP-2003 (first entry)

XX

DE Beta-secretase cleavage site containing oligopeptide substrate.

XX

KW APP; Alzheimer's disease; beta-secretase; beta amyloid peptide; A beta;
 KW amyloid precursor protein; nootropic; neuroprotective.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "N-terminal biotin"

FT Cleavage-site 5. .6

FT /note= "beta-secretase cleavage site"

XX

PN WO2003045378-A1.

XX

PD 05-JUN-2003.

XX

PF 21-NOV-2002; 2002WO-US037360.

XX

PR 21-NOV-2001; 2001US-0334692P.

XX

PA (ELAN-) ELAN PHARM INC.

PA (PHAA) PHARMACIA & UPJOHN CO.

XX

PI John V;

XX

DR WPI; 2003-577200/54.
 XX
 PT Use of amino acid derivatives for e.g. treating mild cognitive impairment
 PT and treating, preventing or delaying the onset of the Alzheimer's
 PT disease.
 XX
 PS Example D; Page 53; 204pp; English.
 XX
 CC The invention relates to the treatment of Alzheimer's disease (AD) and
 CC involves administration of amino acid derivatives of specified formula.
 CC The derivatives act as inhibitors of beta-secretase and inhibits the
 CC production and deposition of beta Amyloid peptide (A beta). They also
 CC inhibit the cleavage of amyloid precursor protein (APP). The derivatives
 CC can be used for treating, preventing or delaying the onset of AD, for
 CC treating mild cognitive impairment (MCI) and preventing or delaying the
 CC onset of AD in those who would progress from MCI to AD; treating Down's
 CC syndrome, hereditary cerebral haemorrhage with amyloidosis of the Dutch-
 CC type, cerebral amyloid angiopathy and preventing its potential
 CC consequences i.e. single and recurrent lobar haemorrhages, other
 CC degenerative dementias (including dementias of mixed vascular and
 CC degenerative origin, dementia associated with Parkinson's disease,
 CC dementia associated with progressive supranuclear palsy, dementia
 CC associated with cortical basal degeneration) or diffuse Lewy body type of
 CC Alzheimer's disease. The present sequence represents a synthetic
 CC oligopeptide substrate containing the known beta-secretase cleavage site,
 CC used to assay beta-secretase activity
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 8; DB 6; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAEF 8
 |||||
 Db 2 EVNLDAEF 9

RESULT 34

ABR56195

ID ABR56195 standard; peptide; 9 AA.

XX

AC ABR56195;

XX

DT 18-DEC-2003 (first entry)

XX

DE Amyloid precursor protein, APP, substrate #7.

XX

KW APP; nootropic; neuroprotective; cerebroprotective; haemostatic;

KW Alzheimer's disease; beta-secretase; Amyloid Precursor Protein; APP;

KW degenerative dementia.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "N-terminal Biotin"

FT Cleavage-site 5. .6
 XX
 PN WO2003037325-A1.
 XX
 PD 08-MAY-2003.
 XX
 PF 29-OCT-2002; 2002WO-US034678.
 XX
 PR 29-OCT-2001; 2001US-0351152P.
 XX
 PA (ELAN-) ELAN PHARM INC.
 PA (PHAA) PHARMACIA & UPJOHN CO.
 XX
 PI Beck JP;
 XX
 DR WPI; 2003-482086/45.
 XX
 PT Treating e.g. Alzheimer's disease, mild cognitive impairment, Down's
 PT syndrome and cerebral amyloid angiopathy comprises administering hydroxy
 PT substituted amide compounds.
 XX
 PS Example D; Page 67; 90pp; English.
 XX
 CC The present invention relates to a method for treating or preventing
 CC Alzheimer's disease. The method comprises administering hydroxy
 CC substituted amide compounds. The compounds inhibit beta-secretase, which
 CC cleaves Amyloid Precursor Protein (APP) to produce A beta protein, a
 CC major component of the amyloid plaques found in the brains of Alzheimer's
 CC sufferers. The method is also useful for treating mild cognitive
 CC impairment, Down's disease, hereditary cerebral haemorrhage with
 CC amyloidosis of the Dutch-type, cerebral amyloid angiopathy and other
 CC degenerative dementias. The present sequence is a synthetic APP substrate
 CC which can be cleaved by beta-secretase. This peptide was used to assay
 CC beta-secretase activity in the presence or absence of the inhibitory
 CC compounds of the invention
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 8; DB 7; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAEF 8
 | | | | | | | |
 Db 2 EVNLDAEF 9

RESULT 35

ADC29723

ID ADC29723 standard; peptide; 9 AA.

XX

AC ADC29723;

XX

DT 18-DEC-2003 (first entry)

XX

DE Synthetic beta-secretase oligopeptide substrate #1.

XX

OM protein - protein search, using sw model

Run on: March 26, 2004, 15:35:53 ; Search time 35.5 Seconds
(without alignments)
58.966 Million cell updates/sec

Title: US-09-668-314C-71
Perfect score: 8
Sequence: 1 EVNLDAEF 8

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1065169 seqs, 261661801 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1065169

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Listing first 1000 summaries

Database : Published Applications AA:*
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13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
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16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Match	Length	DB	ID	Description
No.							

1	8	100.0	9	9	US-09-896-874-8	Sequence 8, Appli
2	8	100.0	9	9	US-09-896-139-8	Sequence 8, Appli
3	8	100.0	9	9	US-09-895-843-8	Sequence 8, Appli
4	8	100.0	9	10	US-09-895-871-8	Sequence 8, Appli
5	8	100.0	9	12	US-10-299-739-8	Sequence 8, Appli
6	8	100.0	9	14	US-10-192-625-8	Sequence 8, Appli
7	8	100.0	9	14	US-10-192-424-8	Sequence 8, Appli
8	8	100.0	9	14	US-10-183-126A-8	Sequence 8, Appli
9	8	100.0	9	14	US-10-171-343-8	Sequence 8, Appli
10	8	100.0	9	14	US-10-264-707-8	Sequence 8, Appli
11	8	100.0	9	14	US-10-066-319-4	Sequence 4, Appli
12	8	100.0	9	14	US-10-337-075-8	Sequence 8, Appli
13	8	100.0	9	14	US-10-160-777-8	Sequence 8, Appli
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17	8	100.0	10	9	US-09-794-743-63	Sequence 63, Appl
18	8	100.0	10	9	US-09-794-748-63	Sequence 63, Appl
19	8	100.0	10	9	US-09-796-264-5	Sequence 5, Appli
20	8	100.0	10	9	US-09-794-925-63	Sequence 63, Appl
21	8	100.0	10	9	US-09-681-442-63	Sequence 63, Appl
22	8	100.0	10	9	US-09-845-226-5	Sequence 5, Appli
23	8	100.0	10	9	US-09-795-903A-5	Sequence 5, Appli
24	8	100.0	10	10	US-09-869-414-63	Sequence 63, Appl
25	8	100.0	10	10	US-09-548-366-63	Sequence 63, Appl
26	8	100.0	10	12	US-10-652-927-63	Sequence 63, Appl
27	8	100.0	10	12	US-10-652-830-63	Sequence 63, Appl
28	8	100.0	10	14	US-10-032-818-8	Sequence 8, Appli
29	8	100.0	10	14	US-10-050-200-22	Sequence 22, Appl
30	8	100.0	11	14	US-10-354-955-2	Sequence 2, Appli
31	8	100.0	11	14	US-10-354-955-4	Sequence 4, Appli
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33	8	100.0	12	9	US-09-896-139-1	Sequence 1, Appli
34	8	100.0	12	9	US-09-895-843-1	Sequence 1, Appli
35	8	100.0	12	10	US-09-895-871-1	Sequence 1, Appli
36	8	100.0	12	14	US-10-032-818-26	Sequence 26, Appl
37	8	100.0	12	15	US-10-400-273-3	Sequence 3, Appli
38	8	100.0	13	12	US-10-299-739-1	Sequence 1, Appli
39	8	100.0	13	14	US-10-192-625-1	Sequence 1, Appli
40	8	100.0	13	14	US-10-192-424-1	Sequence 1, Appli
41	8	100.0	13	14	US-10-183-126A-1	Sequence 1, Appli
42	8	100.0	13	14	US-10-171-343-1	Sequence 1, Appli
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45	8	100.0	13	14	US-10-160-777-1	Sequence 1, Appli
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66	8	100.0	32	10	US-09-895-871-4	Sequence 4, Appli
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74	8	100.0	33	14	US-10-183-126A-6	Sequence 6, Appli
75	8	100.0	33	14	US-10-171-343-6	Sequence 6, Appli
76	8	100.0	33	14	US-10-264-707-6	Sequence 6, Appli
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88	8	100.0	34	15	US-10-192-543-4	Sequence 4, Appli
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92	8	100.0	695	9	US-09-794-748-12	Sequence 12, Appl
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94	8	100.0	695	9	US-09-681-442-12	Sequence 12, Appl
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96	8	100.0	695	10	US-09-548-366-12	Sequence 12, Appl
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98	8	100.0	695	12	US-10-652-830-12	Sequence 12, Appl
99	8	100.0	695	15	US-10-427-208-46	Sequence 46, Appl
100	8	100.0	697	9	US-09-794-927-18	Sequence 18, Appl
101	8	100.0	697	9	US-09-795-847-18	Sequence 18, Appl
102	8	100.0	697	9	US-09-794-743-18	Sequence 18, Appl
103	8	100.0	697	9	US-09-794-748-18	Sequence 18, Appl
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105	8	100.0	697	9	US-09-681-442-18	Sequence 18, Appl
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116	5	62.5	12	15	US-10-457-839-85	Sequence 85, Appl
117	5	62.5	14	15	US-10-457-839-86	Sequence 86, Appl
118	5	62.5	16	15	US-10-457-839-87	Sequence 87, Appl
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132	5	62.5	104	9	US-09-823-153-4	Sequence 4, Appli
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677	5	62.5	281	12	US-10-425-114-57770	Sequence 57770, A
678	5	62.5	284	15	US-10-094-749-1650	Sequence 1650, Ap
679	5	62.5	286	12	US-10-425-114-37667	Sequence 37667, A
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681	5	62.5	295	14	US-10-156-761-15003	Sequence 15003, A
682	5	62.5	305	12	US-10-424-599-189304	Sequence 189304,
683	5	62.5	308	15	US-10-369-493-12074	Sequence 12074, A

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688	5	62.5	331	12	US-10-282-122A-72530	Sequence 72530, A
689	5	62.5	331	16	US-10-389-566-415	Sequence 415, App
690	5	62.5	335	16	US-10-389-566-714	Sequence 714, App
691	5	62.5	336	12	US-10-424-599-145177	Sequence 145177,
692	5	62.5	339	12	US-10-425-114-52515	Sequence 52515, A
693	5	62.5	348	15	US-10-369-493-15493	Sequence 15493, A
694	5	62.5	348	15	US-10-369-493-15864	Sequence 15864, A
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696	5	62.5	350	15	US-10-108-260A-3875	Sequence 3875, Ap
697	5	62.5	351	15	US-10-369-493-16239	Sequence 16239, A
698	5	62.5	351	15	US-10-369-493-16377	Sequence 16377, A
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706	5	62.5	361	12	US-10-425-114-69382	Sequence 69382, A
707	5	62.5	370	16	US-10-389-566-722	Sequence 722, App
708	5	62.5	372	15	US-10-369-493-10211	Sequence 10211, A
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710	5	62.5	379	12	US-10-282-122A-44924	Sequence 44924, A
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712	5	62.5	381	14	US-10-156-761-11475	Sequence 11475, A
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723	5	62.5	397	12	US-10-282-122A-69113	Sequence 69113, A
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758	5	62.5	491	15	US-10-369-493-7380	Sequence 7380, Ap
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778	5	62.5	580	15	US-10-369-493-1328	Sequence 1328, Ap
779	5	62.5	581	14	US-10-156-761-9697	Sequence 9697, Ap
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803	5	62.5	693	9	US-09-984-198-154	Sequence 154, App
804	5	62.5	693	12	US-10-424-599-268383	Sequence 268383,
805	5	62.5	693	12	US-10-425-114-45527	Sequence 45527, A
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826	5	62.5	825	14	US-10-128-714-8429	Sequence 8429, Ap
827	5	62.5	827	14	US-10-101-464A-915	Sequence 915, App
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848	5	62.5	1049	15	US-10-236-031B-52	Sequence 52, Appl
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851	5	62.5	1049	15	US-10-295-027-1166	Sequence 1166, Ap
852	5	62.5	1049	15	US-10-301-330-2	Sequence 2, Appli
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857	5	62.5	1090	12	US-10-276-774-2321	Sequence 2321, Ap
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859	5	62.5	1132	15	US-10-289-762-466	Sequence 466, App
860	5	62.5	1167	15	US-10-369-493-11929	Sequence 11929, A
861	5	62.5	1178	12	US-10-282-122A-72168	Sequence 72168, A
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870	5	62.5	1453	14	US-10-128-714-8549	Sequence 8549, Ap
871	5	62.5	1993	13	US-10-098-979-2	Sequence 2, Appli
872	5	62.5	2696	14	US-10-309-933-4	Sequence 4, Appli
873	5	62.5	2701	14	US-10-171-311-83	Sequence 83, Appl
874	5	62.5	2756	14	US-10-331-061-7	Sequence 7, Appli
875	5	62.5	3450	15	US-10-369-493-5247	Sequence 5247, Ap
876	5	62.5	3450	15	US-10-369-493-5249	Sequence 5249, Ap
877	5	62.5	3461	15	US-10-369-493-5248	Sequence 5248, Ap
878	5	62.5	3461	15	US-10-369-493-5250	Sequence 5250, Ap
879	5	62.5	3562	15	US-10-341-434-109	Sequence 109, App
880	5	62.5	4342	9	US-09-815-242-5107	Sequence 5107, Ap
881	5	62.5	4342	12	US-10-282-122A-43424	Sequence 43424, A
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883	4	50.0	4	9	US-09-795-847-66	Sequence 66, Appl
884	4	50.0	4	9	US-09-794-743-66	Sequence 66, Appl
885	4	50.0	4	9	US-09-794-748-66	Sequence 66, Appl
886	4	50.0	4	9	US-09-794-925-66	Sequence 66, Appl
887	4	50.0	4	9	US-09-681-442-66	Sequence 66, Appl
888	4	50.0	4	10	US-09-869-414-66	Sequence 66, Appl
889	4	50.0	4	12	US-10-652-927-66	Sequence 66, Appl
890	4	50.0	4	12	US-10-652-830-66	Sequence 66, Appl
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894	4	50.0	5	9	US-09-794-927-73	Sequence 73, Appl
895	4	50.0	5	9	US-09-795-847-72	Sequence 72, Appl
896	4	50.0	5	9	US-09-795-847-73	Sequence 73, Appl
897	4	50.0	5	9	US-09-794-743-72	Sequence 72, Appl
898	4	50.0	5	9	US-09-794-743-73	Sequence 73, Appl
899	4	50.0	5	9	US-09-794-748-72	Sequence 72, Appl
900	4	50.0	5	9	US-09-794-748-73	Sequence 73, Appl
901	4	50.0	5	9	US-09-794-925-72	Sequence 72, Appl
902	4	50.0	5	9	US-09-794-925-73	Sequence 73, Appl
903	4	50.0	5	9	US-09-681-442-72	Sequence 72, Appl
904	4	50.0	5	9	US-09-681-442-73	Sequence 73, Appl
905	4	50.0	5	10	US-09-869-414-72	Sequence 72, Appl
906	4	50.0	5	10	US-09-869-414-73	Sequence 73, Appl
907	4	50.0	5	12	US-10-652-927-72	Sequence 72, Appl
908	4	50.0	5	12	US-10-652-927-73	Sequence 73, Appl
909	4	50.0	5	12	US-10-652-830-72	Sequence 72, Appl
910	4	50.0	5	12	US-10-652-830-73	Sequence 73, Appl
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914	4	50.0	6	14	US-10-084-380A-6	Sequence 6, Appli
915	4	50.0	7	9	US-09-867-847-5	Sequence 5, Appli
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917	4	50.0	7	14	US-10-337-970-8	Sequence 8, Appli
918	4	50.0	7	14	US-10-293-580-44	Sequence 44, Appl
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920	4	50.0	8	9	US-09-795-847-67	Sequence 67, Appl
921	4	50.0	8	9	US-09-794-743-67	Sequence 67, Appl
922	4	50.0	8	9	US-09-794-748-67	Sequence 67, Appl
923	4	50.0	8	9	US-09-796-264-28	Sequence 28, Appl
924	4	50.0	8	9	US-09-794-925-67	Sequence 67, Appl
925	4	50.0	8	9	US-09-681-442-67	Sequence 67, Appl
926	4	50.0	8	9	US-09-149-718-10	Sequence 10, Appl
927	4	50.0	8	9	US-09-845-226-28	Sequence 28, Appl
928	4	50.0	8	9	US-09-795-903A-28	Sequence 28, Appl
929	4	50.0	8	10	US-09-869-414-67	Sequence 67, Appl
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931	4	50.0	8	12	US-10-652-830-67	Sequence 67, Appl
932	4	50.0	8	14	US-10-084-380A-3	Sequence 3, Appli
933	4	50.0	8	14	US-10-032-818-5	Sequence 5, Appli
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935	4	50.0	8	15	US-10-427-208-52	Sequence 52, Appl
936	4	50.0	9	13	US-10-016-717-6	Sequence 6, Appli
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938	4	50.0	9	14	US-10-032-818-69	Sequence 69, Appl
939	4	50.0	9	14	US-10-066-319-3	Sequence 3, Appli
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941	4	50.0	9	16	US-10-172-102-109	Sequence 109, App
942	4	50.0	10	9	US-09-794-927-64	Sequence 64, Appl
943	4	50.0	10	9	US-09-795-847-64	Sequence 64, Appl
944	4	50.0	10	9	US-09-794-743-64	Sequence 64, Appl
945	4	50.0	10	9	US-09-794-748-64	Sequence 64, Appl
946	4	50.0	10	9	US-09-796-264-4	Sequence 4, Appli
947	4	50.0	10	9	US-09-794-925-64	Sequence 64, Appl
948	4	50.0	10	9	US-09-681-442-64	Sequence 64, Appl
949	4	50.0	10	9	US-09-845-226-4	Sequence 4, Appli
950	4	50.0	10	9	US-09-795-903A-4	Sequence 4, Appli
951	4	50.0	10	10	US-09-865-294-69	Sequence 69, Appl
952	4	50.0	10	10	US-09-869-414-64	Sequence 64, Appl
953	4	50.0	10	10	US-09-548-366-64	Sequence 64, Appl
954	4	50.0	10	10	US-09-572-270A-985	Sequence 985, App
955	4	50.0	10	12	US-10-652-927-64	Sequence 64, Appl
956	4	50.0	10	12	US-10-652-830-64	Sequence 64, Appl
957	4	50.0	10	14	US-10-032-818-7	Sequence 7, Appli
958	4	50.0	10	14	US-10-010-942B-33	Sequence 33, Appl
959	4	50.0	10	15	US-10-427-208-53	Sequence 53, Appl
960	4	50.0	10	15	US-10-411-544-24	Sequence 24, Appl
961	4	50.0	11	14	US-10-354-955-1	Sequence 1, Appli
962	4	50.0	11	14	US-10-354-955-3	Sequence 3, Appli
963	4	50.0	11	15	US-10-411-544-23	Sequence 23, Appl
964	4	50.0	12	9	US-09-896-874-2	Sequence 2, Appli
965	4	50.0	12	9	US-09-896-139-2	Sequence 2, Appli
966	4	50.0	12	9	US-09-895-843-2	Sequence 2, Appli
967	4	50.0	12	10	US-09-865-294-68	Sequence 68, Appl
968	4	50.0	12	10	US-09-895-871-2	Sequence 2, Appli

969	4	50.0	12	14	US-10-032-818-25	Sequence 25, Appl
970	4	50.0	12	14	US-10-032-818-27	Sequence 27, Appl
971	4	50.0	12	14	US-10-032-818-28	Sequence 28, Appl
972	4	50.0	12	14	US-10-032-818-29	Sequence 29, Appl
973	4	50.0	12	14	US-10-032-818-30	Sequence 30, Appl
974	4	50.0	12	14	US-10-032-818-31	Sequence 31, Appl
975	4	50.0	12	14	US-10-032-818-32	Sequence 32, Appl
976	4	50.0	12	14	US-10-032-818-33	Sequence 33, Appl
977	4	50.0	12	14	US-10-032-818-34	Sequence 34, Appl
978	4	50.0	12	14	US-10-032-818-35	Sequence 35, Appl
979	4	50.0	12	14	US-10-032-818-36	Sequence 36, Appl
980	4	50.0	12	14	US-10-032-818-37	Sequence 37, Appl
981	4	50.0	12	14	US-10-032-818-38	Sequence 38, Appl
982	4	50.0	12	14	US-10-032-818-39	Sequence 39, Appl
983	4	50.0	12	14	US-10-032-818-40	Sequence 40, Appl
984	4	50.0	12	14	US-10-032-818-41	Sequence 41, Appl
985	4	50.0	12	14	US-10-032-818-42	Sequence 42, Appl
986	4	50.0	12	14	US-10-032-818-43	Sequence 43, Appl
987	4	50.0	12	14	US-10-032-818-44	Sequence 44, Appl
988	4	50.0	12	14	US-10-032-818-45	Sequence 45, Appl
989	4	50.0	12	14	US-10-032-818-56	Sequence 56, Appl
990	4	50.0	12	15	US-10-427-208-54	Sequence 54, Appl
991	4	50.0	13	10	US-09-792-079-2	Sequence 2, Appli
992	4	50.0	13	10	US-09-825-242-2	Sequence 2, Appli
993	4	50.0	13	12	US-10-299-739-2	Sequence 2, Appli
994	4	50.0	13	14	US-10-033-741-68	Sequence 68, Appl
995	4	50.0	13	14	US-10-084-380A-7	Sequence 7, Appli
996	4	50.0	13	14	US-10-192-625-2	Sequence 2, Appli
997	4	50.0	13	14	US-10-192-424-2	Sequence 2, Appli
998	4	50.0	13	14	US-10-183-126A-2	Sequence 2, Appli
999	4	50.0	13	14	US-10-171-343-2	Sequence 2, Appli
1000	4	50.0	13	14	US-10-264-707-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-09-896-874-8

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; Sequence 8, Application US/09896874
; Patent No. US20020016320A1
; GENERAL INFORMATION:
; APPLICANT: Fang, Lawrence Y.
; APPLICANT: John, Varghese
; TITLE OF INVENTION: COMPOUNDS TO TREAT ALZHEIMER'S DISEASE
; FILE REFERENCE: 13615.40USU1
; CURRENT APPLICATION NUMBER: US/09/896,874
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/215,323
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
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; OTHER INFORMATION: Synthetic
US-09-896-874-8

Query Match 100.0%; Score 8; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.6e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAEF 8
| | | | | | | |
Db 2 EVNLDAEF 9

RESULT 2

US-09-896-139-8

; Sequence 8, Application US/09896139

; Patent No. US20020128255A1

; GENERAL INFORMATION:

; APPLICANT: Beck, James P.

; APPLICANT: Fang, Lawrence Y.

; APPLICANT: Freskos, John N.

; APPLICANT: Gailunas, Andrea

; APPLICANT: Hom, Roy

; APPLICANT: Jagodzinska, Barbara

; APPLICANT: John, Varghese

; APPLICANT: Maillaird, Michel

; APPLICANT: Pulley, Shon R.

; APPLICANT: TenBrink, Ruth E.

; TITLE OF INVENTION: COMPOUNDS TO TREAT ALZHEIMER'S DISEASE

; FILE REFERENCE: 13615.25USU4

; CURRENT APPLICATION NUMBER: US/09/896,139

; CURRENT FILING DATE: 2001-06-29

; PRIOR APPLICATION NUMBER: US 60/215,323

; PRIOR FILING DATE: 2000-06-30

; PRIOR APPLICATION NUMBER: US 60/252,736

; PRIOR FILING DATE: 2000-11-22

; PRIOR APPLICATION NUMBER: US 60/255,956

; PRIOR FILING DATE: 2000-12-15

; PRIOR APPLICATION NUMBER: US 60/268,497

; PRIOR FILING DATE: 2001-02-13

; PRIOR APPLICATION NUMBER: US 60/279,779

; PRIOR FILING DATE: 2001-03-29

; PRIOR APPLICATION NUMBER: US 60/295,589

; PRIOR FILING DATE: 2001-06-04

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 8

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic

US-09-896-139-8

Query Match 100.0%; Score 8; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.6e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAEF 8
| | | | | | | |
Db 2 EVNLDAEF 9

RESULT 3

US-09-895-843-8

; Sequence 8, Application US/09895843
; Patent No. US20020143177A1
; GENERAL INFORMATION:
; APPLICANT: Beck, James P.
; APPLICANT: Fang, Lawrence Y.
; APPLICANT: Freskos, John N.
; APPLICANT: Gailunas, Andrea
; APPLICANT: Hom, Roy
; APPLICANT: Jagodizinska, Barbara
; APPLICANT: John, Varghese
; APPLICANT: Maillaird, Michel
; APPLICANT: Pulley, Shon R.
; APPLICANT: TenBrink, Ruth E.
; TITLE OF INVENTION: COMPOUNDS TO TREAT ALZHEIMER'S DISEASE
; FILE REFERENCE: 13615.41USU1
; CURRENT APPLICATION NUMBER: US/09/895,843
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/215,323
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-895-843-8

Query Match 100.0%; Score 8; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.6e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAEF 8
| | | | | | | |
Db 2 EVNLDAEF 9

RESULT 4

US-09-895-871-8

; Sequence 8, Application US/09895871
; Publication No. US20030096864A1
; GENERAL INFORMATION:
; APPLICANT: Fang, Lawrence Y.
; APPLICANT: Hom, Roy
; APPLICANT: John, Varghese
; APPLICANT: Maillaird, Michel
; TITLE OF INVENTION: COMPOUNDS TO TREAT ALZHEIMER'S DISEASE
; FILE REFERENCE: 13615.21USU1
; CURRENT APPLICATION NUMBER: US/09/895,871

; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/215,323
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-895-871-8

Query Match 100.0%; Score 8; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.6e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAEF 8
| | | | | | | |
Db 2 EVNLDAEF 9

RESULT 5

US-10-299-739-8

; Sequence 8, Application US/10299739
; Publication No. US20040039064A1
; GENERAL INFORMATION:
; APPLICANT: Elan Pharmaceuticals, Inc.
; APPLICANT: Pharmacia & Upjohn Company
; APPLICANT: Romero, Arthur G.
; APPLICANT: Schostarez, Heinrich J.
; APPLICANT: Christina, McGrain M.
; TITLE OF INVENTION: Amine 1,2- and 1,3-Diol Compounds
; FILE REFERENCE: 01-1724-B
; CURRENT APPLICATION NUMBER: US/10/299,739
; CURRENT FILING DATE: 2003-11-19
; PRIOR APPLICATION NUMBER: 60/333,081
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/334,000
; PRIOR FILING DATE: 2001-11-18
; PRIOR APPLICATION NUMBER: 60/362,752
; PRIOR FILING DATE: 2002-03-08
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-299-739-8

Query Match 100.0%; Score 8; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.6e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAEF 8

Db |||||
 2 EVNLDAEF 9

RESULT 6

US-10-192-625-8

; Sequence 8, Application US/10192625
; Publication No. US20030083353A1
; GENERAL INFORMATION:
; APPLICANT: Schostarez, Heinrich J.
; APPLICANT: Chrusciel, Robert A
; TITLE OF INVENTION: Diaminediols for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 01-1645-B
; CURRENT APPLICATION NUMBER: US/10/192,625
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: 60/304,305
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/334,480
; PRIOR FILING DATE: 2001-07-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(1)
; OTHER INFORMATION: N-terminal biotin
US-10-192-625-8

Query Match 100.0%; Score 8; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.6e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAEF 8
 |||||
Db 2 EVNLDAEF 9

RESULT 7

US-10-192-424-8

; Sequence 8, Application US/10192424
; Publication No. US20030083356A1
; GENERAL INFORMATION:
; APPLICANT: Schostarez, Heinrich J.
; APPLICANT: Chrusciel, Robert A.
; TITLE OF INVENTION: Statine Derivatives for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 02-154-A
; CURRENT APPLICATION NUMBER: US/10/192,424
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: 60/204,128
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/327,424

; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(1)
; OTHER INFORMATION: N-terminal biotin
US-10-192-424-8

Query Match 100.0%; Score 8; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.6e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAEF 8
| | | | | | | |
Db 2 EVNLDAEF 9

RESULT 8

US-10-183-126A-8

; Sequence 8, Application US/10183126A
; Publication No. US20030083518A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia and Upjohn Company
; APPLICANT: John, Varghese
; APPLICANT: Hom, Roy
; APPLICANT: Tucker, John
; TITLE OF INVENTION: Substituted Alcohols Useful in Treatment of Alzheimer's Disease
; FILE REFERENCE: 01-1704-C
; CURRENT APPLICATION NUMBER: US/10/183,126A
; CURRENT FILING DATE: 2002-09-11
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligopeptides substrate with cleavage site of beta-secr
; OTHER INFORMATION: etase and with optionally detectable tag.
US-10-183-126A-8

Query Match 100.0%; Score 8; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.6e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAEF 8
| | | | | | | |
Db 2 EVNLDAEF 9

RESULT 9

US-10-171-343-8

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; Sequence 8, Application US/10171343
; Publication No. US20030092747A1
; GENERAL INFORMATION:
; APPLICANT: Schostarez, Heinrich J.
; APPLICANT: Chrusciel, Rober A.
; TITLE OF INVENTION: Aminediols for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 01-1644-B
; CURRENT APPLICATION NUMBER: US/10/171,343
; CURRENT FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: US 60/297,827
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/333,084
; PRIOR FILING DATE: 2001-11-19
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic peptide
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (1)..(1)
;   OTHER INFORMATION: N-terminal biotin
US-10-171-343-8
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Query Match          100.0%; Score 8; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.6e+05;
Matches      8; Conservative    0; Mismatches    0; Indels      0; Gaps      0;
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Qy      1 EVNLDAEF 8
         |||||
Db      2 EVNLDAEF 9
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RESULT 10

US-10-264-707-8

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; Sequence 8, Application US/10264707
; Publication No. US20030125365A1
; GENERAL INFORMATION:
; APPLICANT: Fisher, Jed F.
; APPLICANT: Jacobs, Jon S.
; APPLICANT: Scherer, Brian S.
; TITLE OF INVENTION: Hydroxypropylamines
; FILE REFERENCE: 01-1555-B
; CURRENT APPLICATION NUMBER: US/10/264,707
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: 60/327,149
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/334,058
; PRIOR FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 9
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(1)
; OTHER INFORMATION: N-terminal biotin
US-10-264-707-8

Query Match 100.0%; Score 8; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.6e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAEF 8
| | | | | | | |
Db 2 EVNLDAEF 9

RESULT 11

US-10-066-319-4

; Sequence 4, Application US/10066319
; Publication No. US20030147810A1
; GENERAL INFORMATION:
; APPLICANT: Ross, Brian D.
; APPLICANT: Rehemtulla, Alnawaz
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REPORTING
; TITLE OF INVENTION: OF PROTEASE ACTIVITY WITHIN THE SECRETORY PATHWAY
; FILE REFERENCE: 11203-007001
; CURRENT APPLICATION NUMBER: US/10/066,319
; CURRENT FILING DATE: 2002-06-17
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-066-319-4

Query Match 100.0%; Score 8; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.6e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAEF 8
| | | | | | | |
Db 2 EVNLDAEF 9

RESULT 12

US-10-337-075-8

; Sequence 8, Application US/10337075
; Publication No. US20030166580A1
; GENERAL INFORMATION:
; APPLICANT: Warpehoski, Martha A.

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; APPLICANT: Jagodzinska, Barbara
; TITLE OF INVENTION: Substituted Amino Carboxamides for the Treatment of
Alzheimer's Disease
; FILE REFERENCE: 01-1795-C
; CURRENT APPLICATION NUMBER: US/10/337,075
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: 60/345,316
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/350,419
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic peptide
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (1)..(1)
;   OTHER INFORMATION: N-terminal biotin
US-10-337-075-8

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Query Match          100.0%; Score 8; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.6e+05;
Matches      8; Conservative    0; Mismatches    0; Indels      0; Gaps      0;

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Qy      1 EVNLDAEF 8
        |||||
Db      2 EVNLDAEF 9

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RESULT 13

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US-10-160-777-8
; Sequence 8, Application US/10160777
; Publication No. US20030166717A1
; GENERAL INFORMATION:
; APPLICANT: Freskos, John
; APPLICANT: Brown, David L.
; APPLICANT: Fobian, Yvette M.
; APPLICANT: Fang, Larry
; APPLICANT: Romero, Arthur G.
; APPLICANT: Varghese, John
; TITLE OF INVENTION: Hydroxy Alkyl Amines
; FILE REFERENCE: 01-1632-C
; CURRENT APPLICATION NUMBER: US/10/160,777
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/343,772
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: 60/332,639
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/295,332
; PRIOR FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8

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; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(1)
; OTHER INFORMATION: N-terminal biotin
US-10-160-777-8

Query Match 100.0%; Score 8; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.6e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAEF 8
| | | | | | | |
Db 2 EVNLDAEF 9

RESULT 14

US-10-192-543-8

; Sequence 8, Application US/10192543
; Publication No. US20040019086A1
; GENERAL INFORMATION:
; APPLICANT: Schostarez, Heinrich J.
; APPLICANT: Chrusciel, Robert A.
; TITLE OF INVENTION: Aminediols for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 02-156-A
; CURRENT APPLICATION NUMBER: US/10/192,543
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: 60/304,129
; PRIOR FILING DATE: 2001-07-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(1)
; OTHER INFORMATION: N-terminal biotin
US-10-192-543-8

Query Match 100.0%; Score 8; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.6e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAEF 8
| | | | | | | |
Db 2 EVNLDAEF 9

RESULT 15

US-09-794-927-63
; Sequence 63, Application US/09794927
; Patent No. US20010016324A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280FG
; CURRENT APPLICATION NUMBER: US/09/794,927
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-794-927-63

Query Match 100.0%; Score 8; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAEF 8
| | | | | | | |
Db 2 EVNLDAEF 9

RESULT 16

US-09-795-847-63
; Sequence 63, Application US/09795847
; Patent No. US20010018208A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
AND

```

; TITLE OF INVENTION:  USES
; TITLE OF INVENTION:  THEREFOR
; FILE REFERENCE:  28341/6280DE
; CURRENT APPLICATION NUMBER:  US/09/795,847
; CURRENT FILING DATE:  2001-02-28
; PRIOR APPLICATION NUMBER:  09/416,901
; PRIOR FILING DATE:  1999-10-13
; PRIOR APPLICATION NUMBER:  60/155,493
; PRIOR FILING DATE:  1999-09-23
; PRIOR APPLICATION NUMBER:  09/404,133
; PRIOR FILING DATE:  1999-09-23
; PRIOR APPLICATION NUMBER:  PCT/US99/20881
; PRIOR FILING DATE:  1999-09-23
; PRIOR APPLICATION NUMBER:  60/101,594
; PRIOR FILING DATE:  1998-09-24
; NUMBER OF SEQ ID NOS:  73
; SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 63
;   LENGTH:  10
;   TYPE:  PRT
;   ORGANISM:  Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION:  Description of Artificial Sequence: synthetic
US-09-795-847-63

```

```

Query Match          100.0%; Score 8; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches      8; Conservative    0; Mismatches    0; Indels      0; Gaps      0;

```

```

QY          1 EVNLDAEF 8
             |||||
Db          2 EVNLDAEF 9

```

RESULT 17

US-09-794-743-63

```

; Sequence 63, Application US/09794743
; Patent No. US20010021391A1
; GENERAL INFORMATION:
; APPLICANT:  Gurney, Mark E.
; APPLICANT:  Bienkowski, Michael J.
; APPLICANT:  Heinrikson, Robert L.
; APPLICANT:  Parodi, Luis A.
; APPLICANT:  Yan, Riqiang
; TITLE OF INVENTION:  ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
AND
; TITLE OF INVENTION:  USES
; TITLE OF INVENTION:  THEREFOR
; FILE REFERENCE:  28341/6280BC
; CURRENT APPLICATION NUMBER:  US/09/794,743
; CURRENT FILING DATE:  2001-02-27
; PRIOR APPLICATION NUMBER:  09/416,901
; PRIOR FILING DATE:  1999-10-13
; PRIOR APPLICATION NUMBER:  60/155,493
; PRIOR FILING DATE:  1999-09-23
; PRIOR APPLICATION NUMBER:  09/404,133
; PRIOR FILING DATE:  1999-09-23

```

; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-794-743-63

Query Match 100.0%; Score 8; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVNLDAEF 8
|||
Db 2 EVNLDAEF 9

RESULT 18

US-09-794-748-63

; Sequence 63, Application US/09794748
; Patent No. US20020037315A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280JL
; CURRENT APPLICATION NUMBER: US/09/794,748
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-794-748-63

Query Match 100.0%; Score 8; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAEF 8
| | | | | | | |
Db 2 EVNLDAEF 9

RESULT 19

US-09-796-264-5

; Sequence 5, Application US/09796264
; Patent No. US20020049303A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Lin, Xinli
; APPLICANT: Koelsch, Gerald
; TITLE OF INVENTION: Catalytically Active Recombinant Memapsin and Methods
; TITLE OF INVENTION: of Use Thereof
; FILE REFERENCE: OMRF 179
; CURRENT APPLICATION NUMBER: US/09/796,264
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/604,608
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/168,060
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: 60/177,836
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/178,368
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/210,292
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-796-264-5

Query Match 100.0%; Score 8; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAEF 8
| | | | | | | |
Db 2 EVNLDAEF 9

RESULT 20

US-09-794-925-63


```

; Sequence 63, Application US/09794925
; Patent No. US20020064819A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280HI
; CURRENT APPLICATION NUMBER: US/09/794,925
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-794-925-63

```

```

Query Match          100.0%; Score 8; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

QY      1 EVNLDAEF 8
        |||||
Db      2 EVNLDAEF 9

```

RESULT 21

US-09-681-442-63

```

; Sequence 63, Application US/09681442
; Patent No. US20020081634A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280FG

```

```

; CURRENT APPLICATION NUMBER: US/09/681,442
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-681-442-63

```

```

Query Match          100.0%; Score 8; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 EVNLD AEF 8
        |||||
Db      2 EVNLD AEF 9

```

RESULT 22

```

US-09-845-226-5
; Sequence 5, Application US/09845226
; Patent No. US20020115600A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Hong, Lin
; APPLICANT: Ghosh, Arun K.
; TITLE OF INVENTION: Inhibitors of Memapsin 2 and Use Thereof
; FILE REFERENCE: OMRF 182
; CURRENT APPLICATION NUMBER: US/09/845,226
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 09/603,713
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/168,060
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: 60/177,836
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/178,368
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/210,292
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 10

```

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-845-226-5

Query Match 100.0%; Score 8; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAEF 8
| | | | | | | |
Db 2 EVNLDAEF 9

RESULT 23

US-09-795-903A-5

; Sequence 5, Application US/09795903A
; Patent No. US20020164760A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Lin, Xinli
; APPLICANT: Koelsch, Gerald
; TITLE OF INVENTION: Catalytically Active Recombinant Memapsin and Methods
; TITLE OF INVENTION: of Use Thereof
; FILE REFERENCE: OMRF 179
; CURRENT APPLICATION NUMBER: US/09/795,903A
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/604,608
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/168,060
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: 60/177,836
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/178,368
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/210,292
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-795-903A-5

Query Match 100.0%; Score 8; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAEF 8
| | | | | | | |
Db 2 EVNLDAEF 9

RESULT 24

US-09-869-414-63

; Sequence 63, Application US/09869414
 ; Publication No. US20030077226A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Beinkowski et al.
 ; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
 AND USES
 ; TITLE OF INVENTION: THEREFOR
 ; FILE REFERENCE: 28341/6280M
 ; CURRENT APPLICATION NUMBER: US/09/869,414
 ; CURRENT FILING DATE: 2001-06-27
 ; PRIOR APPLICATION NUMBER: 09/416,901
 ; PRIOR FILING DATE: 1999-10-13
 ; PRIOR APPLICATION NUMBER: 60/155,493
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: 09/404,133
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: PCT/US99/20881
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: 60/101,594
 ; PRIOR FILING DATE: 1998-09-24
 ; NUMBER OF SEQ ID NOS: 73
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 63
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic
 US-09-869-414-63

Query Match 100.0%; Score 8; DB 10; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.018;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAEF 8
 |||||
 Db 2 EVNLDAEF 9

RESULT 25

US-09-548-366-63

; Sequence 63, Application US/09548366
 ; Publication No. US20030104365A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gurney, Mark E.
 ; APPLICANT: Bienkowski, Michael J.
 ; APPLICANT: Heinrikson, Robert L.
 ; APPLICANT: Parodi, Luis A.
 ; APPLICANT: Yan, Riqiang
 ; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
 AND
 ; TITLE OF INVENTION: USES THEREFOR
 ; FILE REFERENCE: 28341/6280A

```
; CURRENT APPLICATION NUMBER: US/09/548,366
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-548-366-63
```

```
Query Match          100.0%; Score 8; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches      8; Conservative    0; Mismatches    0; Indels      0; Gaps      0;
```

```
Qy      1 EVNLDAEF 8
        |||||
Db      2 EVNLDAEF 9
```

RESULT 26

US-10-652-927-63

```
; Sequence 63, Application US/10652927
; Publication No. US20040043408A1
; GENERAL INFORMATION:
; APPLICANT: Gurney et al.
; TITLE OF INVENTION: Alzheimer's Disease Secretase, APP Substrates Therefor
and Uses
; TITLE OF INVENTION: Therefor
; FILE REFERENCE: 29915/6280N3
; CURRENT APPLICATION NUMBER: US/10/652,927
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: 09/794,925
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 10
```

; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-652-927-63

Query Match 100.0%; Score 8; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAEF 8
| | | | | | | |
Db 2 EVNLDAEF 9

RESULT 27

US-10-652-830-63

; Sequence 63, Application US/10652830
; Publication No. US20040048303A1
; GENERAL INFORMATION:
; APPLICANT: Gurney et al.
; TITLE OF INVENTION: Alzheimer's Disease Secretase, APP Substrates Therefor
and Uses
; TITLE OF INVENTION: Therefor
; FILE REFERENCE: 29915/6280N1
; CURRENT APPLICATION NUMBER: US/10/652,830
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: 09/794,925
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-652-830-63

Query Match 100.0%; Score 8; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAEF 8
| | | | | | | |
Db 2 EVNLDAEF 9

RESULT 28

US-10-032-818-8

```
; Sequence 8, Application US/10032818
; Publication No. US20030092629A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Koelsch, Gerald
; APPLICANT: Ghosh, Arun K.
; TITLE OF INVENTION: Inhibitors of Memapsin 2 and Use Thereof
; FILE REFERENCE: 2932.1006-007
; CURRENT APPLICATION NUMBER: US/10/032,818
; CURRENT FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 60/275,756
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: US 60/258,705
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-032-818-8
```

```
Query Match          100.0%; Score 8; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches      8; Conservative    0; Mismatches    0; Indels      0; Gaps      0;
```

```
Qy      1 EVNLDAEF 8
          |||||
Db      2 EVNLDAEF 9
```

RESULT 29

US-10-050-200-22

```
; Sequence 22, Application US/10050200
; Publication No. US20030166037A1
; GENERAL INFORMATION:
; APPLICANT: Fourie, Anne
; APPLICANT: Coles, Fawn
; APPLICANT: Karlsson, Lars
; TITLE OF INVENTION: Aggreacanase-1 and -2 Peptide Substrates and Methods
; FILE REFERENCE: ORT-1417
; CURRENT APPLICATION NUMBER: US/10/050,200
; CURRENT FILING DATE: 2002-01-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: peptide substrate
US-10-050-200-22
```

Query Match 100.0%; Score 8; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAEF 8
|||||||
Db 3 EVNLDAEF 10

RESULT 30

US-10-354-955-2
; Sequence 2, Application US/10354955
; Publication No. US20030171291A1
; GENERAL INFORMATION:
; APPLICANT: Gary Christie
; APPLICANT: Ishrut Hussain
; APPLICANT: David J. Powell
; TITLE OF INVENTION: No. US20030171291A1 Treatment
; FILE REFERENCE: P32448
; CURRENT APPLICATION NUMBER: US/10/354,955
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: 09/693,744
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 9925136.5
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 11
; TYPE: PRT
; ORGANISM: human
US-10-354-955-2

Query Match 100.0%; Score 8; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAEF 8
|||||||
Db 3 EVNLDAEF 10

RESULT 31

US-10-354-955-4
; Sequence 4, Application US/10354955
; Publication No. US20030171291A1
; GENERAL INFORMATION:
; APPLICANT: Gary Christie
; APPLICANT: Ishrut Hussain
; APPLICANT: David J. Powell
; TITLE OF INVENTION: No. US20030171291A1 Treatment
; FILE REFERENCE: P32448
; CURRENT APPLICATION NUMBER: US/10/354,955
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: 09/693,744
; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 9925136.5
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion protein with maltose binding protein attached at
residue 1'
US-10-354-955-4

Query Match 100.0%; Score 8; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAEF 8
| | | | | | | |
Db 3 EVNLDAEF 10

RESULT 32

US-09-896-874-1
; Sequence 1, Application US/09896874
; Patent No. US20020016320A1
; GENERAL INFORMATION:
; APPLICANT: Fang, Lawrence Y.
; APPLICANT: John, Varghese
; TITLE OF INVENTION: COMPOUNDS TO TREAT ALZHEIMER'S DISEASE
; FILE REFERENCE: 13615.40USU1
; CURRENT APPLICATION NUMBER: US/09/896,874
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/215,323
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-896-874-1

Query Match 100.0%; Score 8; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAEF 8
| | | | | | | |
Db 2 EVNLDAEF 9

RESULT 33

US-09-896-139-1
; Sequence 1, Application US/09896139

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; Patent No. US20020128255A1
; GENERAL INFORMATION:
; APPLICANT: Beck, James P.
; APPLICANT: Fang, Lawrence Y.
; APPLICANT: Freskos, John N.
; APPLICANT: Gailunas, Andrea
; APPLICANT: Hom, Roy
; APPLICANT: Jagodzinska, Barbara
; APPLICANT: John, Varghese
; APPLICANT: Maillaird, Michel
; APPLICANT: Pulley, Shon R.
; APPLICANT: TenBrink, Ruth E.
; TITLE OF INVENTION: COMPOUNDS TO TREAT ALZHEIMER'S DISEASE
; FILE REFERENCE: 13615.25USU4
; CURRENT APPLICATION NUMBER: US/09/896,139
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/215,323
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/252,736
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 60/255,956
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: US 60/268,497
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: US 60/279,779
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: US 60/295,589
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 12
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-09-896-139-1

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Query Match          100.0%; Score 8; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches      8; Conservative    0; Mismatches    0; Indels      0; Gaps      0;

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Qy      1 EVNLDAEF 8
        |||||
Db      2 EVNLDAEF 9

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RESULT 34
US-09-895-843-1
; Sequence 1, Application US/09895843
; Patent No. US20020143177A1
; GENERAL INFORMATION:
; APPLICANT: Beck, James P.
; APPLICANT: Fang, Lawrence Y.
; APPLICANT: Freskos, John N.
; APPLICANT: Gailunas, Andrea
; APPLICANT: Hom, Roy

```

```
; APPLICANT: Jagodizinska, Barbara
; APPLICANT: John, Varghese
; APPLICANT: Maillaird, Michel
; APPLICANT: Pulley, Shon R.
; APPLICANT: TenBrink, Ruth E.
; TITLE OF INVENTION: COMPOUNDS TO TREAT ALZHEIMER'S DISEASE
; FILE REFERENCE: 13615.41USU1
; CURRENT APPLICATION NUMBER: US/09/895,843
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/215,323
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-895-843-1
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Query Match          100.0%; Score 8; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches      8; Conservative    0; Mismatches    0; Indels      0; Gaps      0;
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```
Qy      1 EVNLDAEF 8
        |||||
Db      2 EVNLDAEF 9
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RESULT 35

US-09-895-871-1

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; Sequence 1, Application US/09895871
; Publication No. US20030096864A1
; GENERAL INFORMATION:
; APPLICANT: Fang, Lawrence Y.
; APPLICANT: Hom, Roy
; APPLICANT: John, Varghese
; APPLICANT: Maillaird, Michel
; TITLE OF INVENTION: COMPOUNDS TO TREAT ALZHEIMER'S DISEASE
; FILE REFERENCE: 13615.21USU1
; CURRENT APPLICATION NUMBER: US/09/895,871
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/215,323
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-895-871-1
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Query Match          100.0%; Score 8; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.021;
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Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAEF 8
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Db 2 EVNLDAEF 9

RESULT 36

US-10-032-818-26
 ; Sequence 26, Application US/10032818
 ; Publication No. US20030092629A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Tang, Jordan J.N.
 ; APPLICANT: Koelsch, Gerald
 ; APPLICANT: Ghosh, Arun K.
 ; TITLE OF INVENTION: Inhibitors of Memapsin 2 and Use Thereof
 ; FILE REFERENCE: 2932.1006-007
 ; CURRENT APPLICATION NUMBER: US/10/032,818
 ; CURRENT FILING DATE: 2001-12-28
 ; PRIOR APPLICATION NUMBER: US 60/275,756
 ; PRIOR FILING DATE: 2001-03-14
 ; PRIOR APPLICATION NUMBER: US 60/258,705
 ; PRIOR FILING DATE: 2000-12-28
 ; NUMBER OF SEQ ID NOS: 83
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 26
 ; LENGTH: 12
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic peptide
 US-10-032-818-26

Query Match 100.0%; Score 8; DB 14; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.021;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAEF 8
 |||||

Db 1 EVNLDAEF 8

RESULT 37

US-10-400-273-3
 ; Sequence 3, Application US/10400273
 ; Publication No. US20040014194A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Beyer, Brian
 ; APPLICANT: Hammond, Gerald S
 ; APPLICANT: Reichert, Paul
 ; APPLICANT: Strickland, Corey
 ; APPLICANT: Wang, Wenyan
 ; APPLICANT: Weber, Patricia C
 ; APPLICANT: Wong, Gwendolyn
 ; APPLICANT: Zhang, Lili
 ; TITLE OF INVENTION: BETA-SECRETASE CRYSTALS AND METHODS FOR PREPARING AND
 USING THE SAME

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; FILE REFERENCE: JB01531-K-US
; CURRENT APPLICATION NUMBER: US/10/400,273
; CURRENT FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: 60/367,937
; PRIOR FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cleavage sequence
US-10-400-273-3
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Query Match          100.0%; Score 8; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches      8; Conservative    0; Mismatches    0; Indels    0; Gaps    0;
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```
Qy      1 EVNLDAEF 8
        |||||
Db      3 EVNLDAEF 10
```

RESULT 38

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US-10-299-739-1
; Sequence 1, Application US/10299739
; Publication No. US20040039064A1
; GENERAL INFORMATION:
; APPLICANT: Elan Pharmaceuticals, Inc.
; APPLICANT: Pharmacia & Upjohn Company
; APPLICANT: Romero, Arthur G.
; APPLICANT: Schostarez, Heinrich J.
; APPLICANT: Christina, McGrain M.
; TITLE OF INVENTION: Amine 1,2- and 1,3-Diol Compounds
; FILE REFERENCE: 01-1724-B
; CURRENT APPLICATION NUMBER: US/10/299,739
; CURRENT FILING DATE: 2003-11-19
; PRIOR APPLICATION NUMBER: 60/333,081
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/334,000
; PRIOR FILING DATE: 2001-11-18
; PRIOR APPLICATION NUMBER: 60/362,752
; PRIOR FILING DATE: 2002-03-08
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(1)
; OTHER INFORMATION: N-terminal biotin
; FEATURE:
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; NAME/KEY: MISC_FEATURE
; LOCATION: (11)..(11)
; OTHER INFORMATION: covalent attachment of oregon green
US-10-299-739-1

Query Match 100.0%; Score 8; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAEF 8
| | | | | | | |
Db 2 EVNLDAEF 9

RESULT 39

US-10-192-625-1

; Sequence 1, Application US/10192625
; Publication No. US20030083353A1
; GENERAL INFORMATION:
; APPLICANT: Schostarez, Heinrich J.
; APPLICANT: Chrusciel, Robert A
; TITLE OF INVENTION: Diaminediols for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 01-1645-B
; CURRENT APPLICATION NUMBER: US/10/192,625
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: 60/304,305
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/334,480
; PRIOR FILING DATE: 2001-07-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(1)
; OTHER INFORMATION: N-terminal biotin
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (11)..(11)
; OTHER INFORMATION: covalent attachment of oregon green
US-10-192-625-1

Query Match 100.0%; Score 8; DB 14; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAEF 8
| | | | | | | |
Db 2 EVNLDAEF 9

RESULT 40

US-10-192-424-1
 ; Sequence 1, Application US/10192424
 ; Publication No. US20030083356A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schostarez, Heinrich J.
 ; APPLICANT: Chrusciel, Robert A.
 ; TITLE OF INVENTION: Statine Derivatives for the Treatment of Alzheimer's Disease
 ; FILE REFERENCE: 02-154-A
 ; CURRENT APPLICATION NUMBER: US/10/192,424
 ; CURRENT FILING DATE: 2002-07-10
 ; PRIOR APPLICATION NUMBER: 60/204,128
 ; PRIOR FILING DATE: 2001-07-10
 ; PRIOR APPLICATION NUMBER: 60/327,424
 ; PRIOR FILING DATE: 2001-10-05
 ; NUMBER OF SEQ ID NOS: 9
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 1
 ; LENGTH: 13
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: synthetic peptide
 ; FEATURE:
 ; NAME/KEY: MISC_FEATURE
 ; LOCATION: (1)..(1)
 ; OTHER INFORMATION: N-terminal biotin
 ; FEATURE:
 ; NAME/KEY: MISC_FEATURE
 ; LOCATION: (11)..(11)
 ; OTHER INFORMATION: covalent attachment of oregon green
 US-10-192-424-1

Query Match 100.0%; Score 8; DB 14; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.022;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAEF 8
 |||||
 Db 2 EVNLDAEF 9

Search completed: March 26, 2004, 15:44:15
 Job time : 47.5 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 26, 2004, 15:30:32 ; Search time 36 Seconds
(without alignments)
70.115 Million cell updates/sec

Title: US-09-668-314C-71
Perfect score: 8
Sequence: 1 EVNLDAEF 8

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriaphage:*
17: sp_archaeophages:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	
No.	Score Match Length DB ID	Description

1	6	75.0	54	16	Q8P193	Q8p193 streptococc
2	6	75.0	91	16	Q89LY8	Q89ly8 bradyrhizob
3	6	75.0	101	12	Q80PA8	Q80pa8 spodoptera
4	6	75.0	173	16	Q87ZB6	Q87zb6 pseudomonas
5	6	75.0	221	16	Q82WI7	Q82wi7 nitrosomona
6	6	75.0	281	16	Q8A4M0	Q8a4m0 bacteroides
7	6	75.0	299	2	Q93ET9	Q93et9 escherichia
8	6	75.0	299	2	Q9EVD7	Q9evd7 enterococcu
9	6	75.0	304	2	Q933C0	Q933c0 rhizobium t
10	6	75.0	308	10	Q8H0B0	Q8h0b0 oryza sativ
11	6	75.0	319	16	Q7V5K6	Q7v5k6 prochloroco
12	6	75.0	324	16	Q88P95	Q88p95 pseudomonas
13	6	75.0	324	16	Q7U4X9	Q7u4x9 synechococc
14	6	75.0	326	16	Q9HVV0	Q9hvw0 pseudomonas
15	6	75.0	352	2	Q9AHQ9	Q9ahq9 gamma-prote
16	6	75.0	357	10	Q8H0A8	Q8h0a8 oryza sativ
17	6	75.0	381	10	Q8LNJ6	Q8lnj6 oryza sativ
18	6	75.0	436	13	Q8AVI2	Q8avi2 xenopus lae
19	6	75.0	500	16	Q87UP7	Q87up7 pseudomonas
20	6	75.0	802	17	Q97XQ7	Q97xq7 sulfolobus
21	6	75.0	822	5	Q9VI82	Q9vi82 drosophila
22	6	75.0	839	5	Q96LM8	Q96lm8 drosophila
23	6	75.0	868	16	Q9KRY9	Q9kry9 vibrio chol
24	6	75.0	894	16	Q7WMP8	Q7wmp8 bordetella
25	6	75.0	894	16	Q7WB80	Q7wb80 bordetella
26	6	75.0	1324	16	Q8DL57	Q8dl57 synechococc
27	6	75.0	1469	5	Q8INT5	Q8int5 drosophila
28	6	75.0	4639	5	Q9VZ83	Q9vz83 drosophila
29	6	75.0	4998	11	Q8CG65	Q8cg65 mus musculu
30	5	62.5	46	16	Q88UM4	Q88um4 lactobacill
31	5	62.5	49	13	Q9PVI4	Q9pvi4 gallus gall
32	5	62.5	50	2	Q8KM85	Q8km85 mycoplasma
33	5	62.5	55	16	Q8CKW2	Q8ckw2 yersinia pe
34	5	62.5	63	4	Q8WYE8	Q8weye8 homo sapien
35	5	62.5	66	3	Q96X11	Q96x11 phaeosphaer
36	5	62.5	67	6	Q9TU51	Q9tu51 sus scrofa
37	5	62.5	67	13	Q9IB55	Q9ib55 xenopus lae
38	5	62.5	67	13	Q9IB58	Q9ib58 xenopus lae
39	5	62.5	68	16	Q8CN01	Q8cn01 staphylococ
40	5	62.5	70	1	Q8NKU7	Q8nku7 acidianus a
41	5	62.5	79	2	P96055	P96055 salmonella
42	5	62.5	84	2	Q8KM09	Q8km09 photorhabdu
43	5	62.5	84	13	Q9W7I7	Q9w7i7 gallus gall
44	5	62.5	88	16	Q7UR07	Q7ur07 rhodopirell
45	5	62.5	89	5	Q7YZN2	Q7yzn2 trichomonas
46	5	62.5	91	16	Q8F784	Q8f784 leptospira
47	5	62.5	92	5	Q8IS88	Q8is88 trypanosoma
48	5	62.5	92	5	Q7YZC6	Q7yzc6 trypanosoma
49	5	62.5	92	5	Q7YZC5	Q7yzc5 trypanosoma
50	5	62.5	98	6	Q9MYU9	Q9myu9 canis famil
51	5	62.5	105	3	O13706	O13706 schizosacch
52	5	62.5	105	16	Q8ZQG4	Q8zqg4 salmonella
53	5	62.5	109	16	Q8NT07	Q8nt07 corynebacte
54	5	62.5	109	16	Q8ZQ87	Q8zq87 salmonella
55	5	62.5	110	3	Q12338	Q12338 saccharomyc
56	5	62.5	110	16	Q81L62	Q81l62 bacillus an
57	5	62.5	110	16	Q817L0	Q817l0 bacillus ce

58	5	62.5	110	17	Q8PYI4	Q8pyi4 methanosarc
59	5	62.5	111	2	Q9RIH2	Q9rih2 xenorhabdus
60	5	62.5	111	3	Q86ZQ6	Q86zq6 heterobasid
61	5	62.5	111	3	Q86ZQ5	Q86zq5 heterobasid
62	5	62.5	111	3	Q86ZQ4	Q86zq4 heterobasid
63	5	62.5	111	3	Q86Z67	Q86z67 heterobasid
64	5	62.5	111	5	Q8I176	Q8i176 drosophila
65	5	62.5	112	16	Q8ZN06	Q8zn06 salmonella
66	5	62.5	117	11	Q8BL85	Q8bl85 mus musculu
67	5	62.5	119	5	Q9N4P2	Q9n4p2 caenorhabdi
68	5	62.5	123	10	Q852G9	Q852g9 oryza sativ
69	5	62.5	126	16	Q8Y3M6	Q8y3m6 listeria mo
70	5	62.5	129	2	Q9S3I8	Q9s3i8 haemophilus
71	5	62.5	129	2	O32626	O32626 haemophilus
72	5	62.5	130	2	Q9EWB7	Q9ewb7 streptomyce
73	5	62.5	132	4	Q9HBS8	Q9hbs8 homo sapien
74	5	62.5	132	16	Q8PG55	Q8pg55 xanthomonas
75	5	62.5	133	16	Q81JK5	Q81jk5 bacillus an
76	5	62.5	135	17	O28910	O28910 archaeglob
77	5	62.5	136	17	Q9YBS2	Q9ybs2 aeropyrum p
78	5	62.5	141	16	Q9ANL3	Q9anl3 bradyrhizob
79	5	62.5	142	2	Q9F0I4	Q9f0i4 rhizobium f
80	5	62.5	142	16	P73462	P73462 synechocyst
81	5	62.5	143	4	Q9H935	Q9h935 homo sapien
82	5	62.5	144	16	Q9HVI0	Q9hvi0 pseudomonas
83	5	62.5	146	2	Q7WX31	Q7wx31 alcaligenes
84	5	62.5	147	16	P74066	P74066 synechocyst
85	5	62.5	147	17	Q8TTG1	Q8ttg1 methanosarc
86	5	62.5	148	11	Q9CXA5	Q9cxa5 mus musculu
87	5	62.5	148	16	Q8Y906	Q8y906 listeria mo
88	5	62.5	151	16	Q8ZBQ4	Q8zbq4 yersinia pe
89	5	62.5	156	2	Q8KY19	Q8ky19 pseudomonas
90	5	62.5	156	2	Q8KRE2	Q8kre2 pseudomonas
91	5	62.5	156	16	Q88EB4	Q88eb4 pseudomonas
92	5	62.5	159	2	Q9F8K6	Q9f8k6 carboxydoth
93	5	62.5	166	16	O69720	O69720 mycobacteri
94	5	62.5	168	13	Q7SYI3	Q7syi3 gallus gall
95	5	62.5	168	16	Q9PQB0	Q9pqb0 ureaplasma
96	5	62.5	170	16	Q8KDH8	Q8kdh8 chlorobium
97	5	62.5	170	17	O52035	O52035 halobacteri
98	5	62.5	171	3	Q9HFT2	Q9hft2 coriolopsis
99	5	62.5	172	16	Q9PMA5	Q9pma5 campylobact
100	5	62.5	172	16	Q8CVT1	Q8cvt1 escherichia
101	5	62.5	172	16	Q83K10	Q83k10 shigella fl
102	5	62.5	173	3	Q12408	Q12408 saccharomyc
103	5	62.5	173	16	Q7VFT1	Q7vft1 helicobacte
104	5	62.5	173	16	Q7TVS0	Q7tvs0 mycobacteri
105	5	62.5	174	2	Q9S696	Q9s696 haemophilus
106	5	62.5	174	16	Q8DF31	Q8df31 vibrio vuln
107	5	62.5	178	12	Q98Y37	Q98y37 reptilian p
108	5	62.5	178	12	Q994S6	Q994s6 snake atcc-
109	5	62.5	178	12	Q98Y59	Q98y59 reptilian p
110	5	62.5	178	12	Q994S4	Q994s4 snake atcc-
111	5	62.5	178	12	Q98Y62	Q98y62 reptilian p
112	5	62.5	178	12	Q91T11	Q91t11 reptilian p
113	5	62.5	178	16	Q8A635	Q8a635 bacteroides
114	5	62.5	182	2	Q9S695	Q9s695 haemophilus

115	5	62.5	182	2	Q9S694	Q9s694 haemophilus
116	5	62.5	182	16	O25859	O25859 helicobacte
117	5	62.5	182	16	Q9ZJV8	Q9zjv8 helicobacte
118	5	62.5	183	10	Q7XWX7	Q7xwx7 oryza sativ
119	5	62.5	183	16	Q8NPK2	Q8npg2 corynebacte
120	5	62.5	184	2	Q9S6A0	Q9s6a0 haemophilus
121	5	62.5	184	4	Q9H875	Q9h875 homo sapien
122	5	62.5	185	2	Q9S697	Q9s697 haemophilus
123	5	62.5	185	2	Q9S698	Q9s698 haemophilus
124	5	62.5	186	2	Q9S6A2	Q9s6a2 haemophilus
125	5	62.5	186	11	Q9CWV6	Q9cwv6 mus musculu
126	5	62.5	186	11	Q9CY32	Q9cy32 mus musculu
127	5	62.5	187	12	Q7TLV5	Q7tlv5 choristoneu
128	5	62.5	187	16	Q9RGV1	Q9rgv1 salmonella
129	5	62.5	188	2	O68806	O68806 synechococc
130	5	62.5	188	2	Q9S6A6	Q9s6a6 haemophilus
131	5	62.5	188	2	Q9S6A8	Q9s6a8 haemophilus
132	5	62.5	188	2	Q9S6A9	Q9s6a9 haemophilus
133	5	62.5	188	2	Q9S6A3	Q9s6a3 haemophilus
134	5	62.5	188	2	Q9S6A5	Q9s6a5 haemophilus
135	5	62.5	188	16	Q88DZ7	Q88dz7 pseudomonas
136	5	62.5	189	2	Q9S6A7	Q9s6a7 haemophilus
137	5	62.5	189	2	Q9S6A4	Q9s6a4 haemophilus
138	5	62.5	189	2	Q9S6A1	Q9s6a1 haemophilus
139	5	62.5	192	4	Q8WV02	Q8wv02 homo sapien
140	5	62.5	192	4	Q8WVE9	Q8wve9 homo sapien
141	5	62.5	193	2	Q9X4F4	Q9x4f4 haemophilus
142	5	62.5	193	16	Q9A0N1	Q9a0n1 streptococc
143	5	62.5	193	16	Q8NZS3	Q8nzs3 streptococc
144	5	62.5	193	16	Q938K4	Q938k4 streptococc
145	5	62.5	195	2	Q9S693	Q9s693 haemophilus
146	5	62.5	198	2	Q8KJS9	Q8kjs9 pseudomonas
147	5	62.5	200	16	Q8ZLC5	Q8zlc5 salmonella
148	5	62.5	200	16	Q88HM1	Q88hml pseudomonas
149	5	62.5	200	16	Q8Z280	Q8z280 salmonella
150	5	62.5	203	16	Q7UV97	Q7uv97 rhodopirell
151	5	62.5	204	13	Q9I9D9	Q9i9d9 xenopus lae
152	5	62.5	205	2	Q9RNG7	Q9rng7 legionella
153	5	62.5	206	16	Q82I89	Q82i89 streptomyce
154	5	62.5	208	13	Q7SZC6	Q7szc6 gallus gall
155	5	62.5	208	16	Q92WD5	Q92wd5 rhizobium m
156	5	62.5	208	17	Q8TUQ3	Q8tuq3 methanosarc
157	5	62.5	209	2	Q8GMR9	Q8gmr9 synechococc
158	5	62.5	209	2	Q8GFP4	Q8gfp4 citrobacter
159	5	62.5	209	5	Q9U504	Q9u504 manduca sex
160	5	62.5	210	2	Q8RLA9	Q8rla9 lactobacill
161	5	62.5	210	16	Q88YJ6	Q88yj6 lactobacill
162	5	62.5	211	16	Q8EQ35	Q8eq35 oceanobacil
163	5	62.5	212	2	Q9FA34	Q9fa34 salmonella
164	5	62.5	212	2	Q9K2H0	Q9k2h0 streptococc
165	5	62.5	212	16	Q9RT20	Q9rt20 deinococcus
166	5	62.5	212	16	Q8EEW7	Q8eew7 shewanella
167	5	62.5	212	17	Q8PX99	Q8px99 methanosarc
168	5	62.5	214	10	Q7XVQ9	Q7xvq9 oryza sativ
169	5	62.5	214	16	Q9ABK9	Q9abk9 caulobacter
170	5	62.5	216	10	Q9FY89	Q9fy89 arabidopsis
171	5	62.5	217	16	Q8XBX3	Q8xbx3 escherichia

172	5	62.5	217	16	Q8Z8M5	Q8z8m5	salmonella
173	5	62.5	217	16	Q7UDG3	Q7udg3	shigella fl
174	5	62.5	219	2	Q9X5A5	Q9x5a5	treponema d
175	5	62.5	222	16	Q9HWM7	Q9hwm7	pseudomonas
176	5	62.5	226	17	Q8TP55	Q8tp55	methanosarc
177	5	62.5	227	2	O87933	O87933	streptococc
178	5	62.5	227	16	Q8R798	Q8r798	thermoanaer
179	5	62.5	228	5	Q86ML6	Q86ml6	drosophila
180	5	62.5	228	8	Q7Y8X0	Q7y8x0	portunus tr
181	5	62.5	228	10	Q7XKU0	Q7xku0	oryza sativ
182	5	62.5	228	16	Q97MP4	Q97mp4	clostridium
183	5	62.5	230	16	Q8DCR4	Q8dcr4	vibrio vuln
184	5	62.5	231	16	Q98HL6	Q98hl6	rhizobium l
185	5	62.5	232	16	Q9ZHS1	Q9zhs1	brucella ab
186	5	62.5	232	16	Q8FZ93	Q8fz93	brucella su
187	5	62.5	232	17	Q8TJF1	Q8tjf1	methanosarc
188	5	62.5	233	2	Q84DC5	Q84dc5	pseudomonas
189	5	62.5	233	9	O80122	O80122	bacterioph
190	5	62.5	233	16	Q9FD95	Q9fd95	rhizobium m
191	5	62.5	234	16	Q8UCP9	Q8ucp9	agrobacteri
192	5	62.5	235	10	Q8S3V0	Q8s3v0	sandersonia
193	5	62.5	235	16	Q87AL8	Q87al8	xylella fas
194	5	62.5	235	16	Q7UII5	Q7uii5	rhodopirell
195	5	62.5	237	2	Q9RNH4	Q9rnh4	rhodobacter
196	5	62.5	237	10	Q9FMM5	Q9fmm5	arabidopsis
197	5	62.5	237	17	Q97UC2	Q97uc2	sulfolobus
198	5	62.5	238	16	Q87L39	Q87l39	vibrio para
199	5	62.5	239	16	Q92L63	Q92l63	rhizobium m
200	5	62.5	239	16	Q7UFQ9	Q7ufq9	rhodopirell
201	5	62.5	239	16	Q7TXW2	Q7txw2	mycobacteri
202	5	62.5	240	16	Q9KV03	Q9kv03	vibrio chol
203	5	62.5	240	16	Q81VD4	Q81vd4	bacillus an
204	5	62.5	240	16	Q81IR5	Q81ir5	bacillus ce
205	5	62.5	242	16	Q988K7	Q988k7	rhizobium l
206	5	62.5	246	16	Q8UA44	Q8ua44	agrobacteri
207	5	62.5	251	16	Q7UYX9	Q7uyx9	rhodopirell
208	5	62.5	252	2	Q44226	Q44226	anabaena sp
209	5	62.5	254	16	Q8YKI8	Q8yki8	anabaena sp
210	5	62.5	254	16	Q8E6W0	Q8e6w0	streptococc
211	5	62.5	256	16	Q8XID9	Q8xid9	clostridium
212	5	62.5	257	11	Q8C270	Q8c270	mus musculu
213	5	62.5	258	2	Q9ZB90	Q9zb90	mycobacteri
214	5	62.5	259	10	Q9ZS05	Q9zs05	arabidopsis
215	5	62.5	259	11	Q9D5K1	Q9d5k1	mus musculu
216	5	62.5	259	13	Q7SYP7	Q7syp7	xenopus lae
217	5	62.5	262	2	Q50381	Q50381	mycobacteri
218	5	62.5	263	10	Q8L583	Q8l583	oryza sativ
219	5	62.5	264	16	Q8YF10	Q8yf10	brucella me
220	5	62.5	264	16	Q8G2T0	Q8g2t0	brucella su
221	5	62.5	264	16	Q82SU9	Q82su9	nitrosomona
222	5	62.5	265	16	Q93RU8	Q93ru8	streptomyce
223	5	62.5	266	12	Q9Q8F3	Q9q8f3	myxoma viru
224	5	62.5	266	12	O41507	O41507	myxoma viru
225	5	62.5	271	11	Q8C1K7	Q8clk7	mus musculu
226	5	62.5	271	11	Q99JJ9	Q99jj9	mus musculu
227	5	62.5	273	13	Q7ZYS3	Q7zys3	xenopus lae
228	5	62.5	278	16	Q9WY10	Q9wy10	thermotoga

229	5	62.5	280	10	Q9SU75	Q9su75 arabidopsis
230	5	62.5	282	3	Q872W3	Q872w3 neurospora
231	5	62.5	282	5	O02335	O02335 caenorhabdi
232	5	62.5	282	16	Q8EE61	Q8ee61 shewanella
233	5	62.5	283	11	Q8C619	Q8c619 mus musculu
234	5	62.5	283	13	Q7SYI2	Q7syi2 gallus gall
235	5	62.5	284	4	Q96NV5	Q96nv5 homo sapien
236	5	62.5	286	2	Q84FA4	Q84fa4 myxococcus
237	5	62.5	286	16	Q8A1T0	Q8alt0 bacteroides
238	5	62.5	287	10	Q8RUH6	Q8ruh6 oryza sativ
239	5	62.5	287	16	Q88JU0	Q88ju0 pseudomonas
240	5	62.5	287	17	Q8U2G0	Q8u2g0 pyrococcus
241	5	62.5	288	17	Q8TKG8	Q8tkg8 methanosarc
242	5	62.5	289	3	O59753	O59753 schizosacch
243	5	62.5	291	10	O22239	O22239 arabidopsis
244	5	62.5	292	16	Q930N1	Q930n1 rhizobium m
245	5	62.5	292	16	Q97D33	Q97d33 clostridium
246	5	62.5	293	16	Q89SE3	Q89se3 bradyrhizob
247	5	62.5	293	16	Q821R7	Q821r7 chlamydophi
248	5	62.5	293	16	Q7UIT1	Q7uit1 rhodopirell
249	5	62.5	295	2	Q8GF30	Q8gf30 zymomonas m
250	5	62.5	295	16	Q825I2	Q825i2 streptomyce
251	5	62.5	296	5	Q9I7I1	Q9i7i1 drosophila
252	5	62.5	296	16	Q7WM54	Q7wm54 bordetella
253	5	62.5	296	16	Q7W8J1	Q7w8j1 bordetella
254	5	62.5	296	17	Q8PS23	Q8ps23 methanosarc
255	5	62.5	297	12	Q91PC0	Q91pc0 human enter
256	5	62.5	298	2	Q9REN4	Q9ren4 zymomonas m
257	5	62.5	299	10	Q851G0	Q851g0 oryza sativ
258	5	62.5	300	2	Q9X486	Q9x486 lactococcus
259	5	62.5	306	10	Q8W0D0	Q8w0d0 oryza sativ
260	5	62.5	308	4	Q8N723	Q8n723 homo sapien
261	5	62.5	308	16	Q98DW2	Q98dw2 rhizobium l
262	5	62.5	308	17	Q97VU0	Q97vu0 sulfolobus
263	5	62.5	310	16	Q98K69	Q98k69 rhizobium l
264	5	62.5	312	16	Q89GC4	Q89gc4 bradyrhizob
265	5	62.5	313	16	Q9RUL3	Q9rul3 deinococcus
266	5	62.5	315	4	Q8NFV4	Q8nfv4 homo sapien
267	5	62.5	317	5	Q23076	Q23076 caenorhabdi
268	5	62.5	317	16	Q9CK47	Q9ck47 pasteurella
269	5	62.5	319	2	Q8KVR3	Q8kvr3 streptococc
270	5	62.5	319	2	Q56043	Q56043 streptococc
271	5	62.5	319	4	Q8NFN6	Q8nfn6 homo sapien
272	5	62.5	319	16	Q8DEE5	Q8dee5 vibrio vuln
273	5	62.5	319	16	Q87SS2	Q87ss2 vibrio para
274	5	62.5	320	16	Q89MH6	Q89mh6 bradyrhizob
275	5	62.5	320	16	Q7U8H6	Q7u8h6 synechococc
276	5	62.5	321	16	Q9KP88	Q9kp88 vibrio chol
277	5	62.5	323	17	Q8PXN5	Q8pxn5 methanosarc
278	5	62.5	324	2	Q8KLW6	Q8klw6 pseudomonas
279	5	62.5	324	2	Q44016	Q44016 alcaligenes
280	5	62.5	326	3	O74553	O74553 schizosacch
281	5	62.5	326	13	Q9I9B2	Q9i9b2 xenopus lae
282	5	62.5	328	10	Q93XG1	Q93xg1 zea mays (m
283	5	62.5	329	11	Q9JI84	Q9ji84 mus musculu
284	5	62.5	329	16	Q8FT63	Q8ft63 corynebacte
285	5	62.5	330	12	Q9YTK5	Q9ytk5 ateline her

286	5	62.5	330	12	Q80BL8	Q80bl8	saimiriine
287	5	62.5	330	16	Q8PQH3	Q8pqh3	xanthomonas
288	5	62.5	331	11	Q91ZF2	Q91zf2	mus musculus
289	5	62.5	332	5	Q8SXG8	Q8sxcg8	drosophila
290	5	62.5	333	10	Q8S1Q9	Q8slq9	oryza sativ
291	5	62.5	333	16	Q7WIZ4	Q7wiz4	bordetella
292	5	62.5	334	11	Q920D9	Q920d9	rattus norv
293	5	62.5	336	15	Q98YA3	Q98ya3	human immun
294	5	62.5	337	3	Q9C1F0	Q9clf0	thanatephor
295	5	62.5	337	16	Q8DWD6	Q8dwd6	streptococc
296	5	62.5	339	12	Q919S4	Q919s4	white spot
297	5	62.5	339	16	Q8PK45	Q8pk45	xanthomonas
298	5	62.5	339	16	Q8P8L3	Q8p8l3	xanthomonas
299	5	62.5	341	5	Q9XUD6	Q9xud6	caenorhabdi
300	5	62.5	341	16	Q986V8	Q986v8	rhizobium l
301	5	62.5	342	5	Q86EH1	Q86ehl	schistosoma
302	5	62.5	343	3	Q9C0Q5	Q9c0q5	thanatephor
303	5	62.5	343	10	Q8RW34	Q8rw34	lycopersico
304	5	62.5	343	10	Q9AVR9	Q9avr9	pisum sativ
305	5	62.5	343	16	Q8YAM9	Q8yam9	listeria mo
306	5	62.5	343	16	Q884I7	Q884i7	pseudomonas
307	5	62.5	344	3	Q9C1F1	Q9clf1	thanatephor
308	5	62.5	344	5	Q26655	Q26655	sarcophaga
309	5	62.5	344	16	Q9JZ80	Q9jz80	neisseria m
310	5	62.5	344	16	Q9JUA2	Q9jua2	neisseria m
311	5	62.5	344	16	Q7W6W5	Q7w6w5	bordetella
312	5	62.5	346	16	Q7VGP4	Q7vgp4	helicobacte
313	5	62.5	346	17	Q8PTC7	Q8ptc7	methanosarc
314	5	62.5	347	12	Q9YWP5	Q9ywp5	kadipiro vi
315	5	62.5	348	16	Q9KC20	Q9kc20	bacillus ha
316	5	62.5	349	5	Q9N8J9	Q9n8j9	trypanosoma
317	5	62.5	350	2	Q8KWB5	Q8kwb5	ruegeria sp
318	5	62.5	350	16	Q9RT72	Q9rt72	deinococcus
319	5	62.5	350	17	Q9V2L3	Q9v2l3	pyrococcus
320	5	62.5	351	16	Q8PGN1	Q8pgn1	xanthomonas
321	5	62.5	354	16	Q8Z1E9	Q8z1e9	salmonella
322	5	62.5	357	16	Q8UBB3	Q8ubb3	agrobacteri
323	5	62.5	357	16	Q831F6	Q831f6	enterococcu
324	5	62.5	357	17	Q9HR66	Q9hr66	halobacteri
325	5	62.5	358	16	Q92XF6	Q92xf6	rhizobium m
326	5	62.5	359	10	Q42809	Q42809	glycine max
327	5	62.5	359	16	Q989G1	Q989g1	rhizobium l
328	5	62.5	360	16	Q8ZMT2	Q8zmt2	salmonella
329	5	62.5	360	16	Q92T68	Q92t68	rhizobium m
330	5	62.5	360	16	Q8PH74	Q8ph74	xanthomonas
331	5	62.5	360	16	Q8P5V3	Q8p5v3	xanthomonas
332	5	62.5	361	16	Q92TH6	Q92th6	rhizobium m
333	5	62.5	361	16	Q8UB69	Q8ub69	agrobacteri
334	5	62.5	361	16	Q8G501	Q8g501	bifidobacte
335	5	62.5	362	16	Q92UQ0	Q92uq0	rhizobium m
336	5	62.5	365	16	Q8EV30	Q8ev30	mycoplasma
337	5	62.5	365	16	Q89PB2	Q89pb2	bradyrhizob
338	5	62.5	366	16	Q8ZHN3	Q8zhn3	yersinia pe
339	5	62.5	366	16	Q8XMX2	Q8xmx2	clostridium
340	5	62.5	367	16	Q8UBA5	Q8uba5	agrobacteri
341	5	62.5	367	16	Q8G0H6	Q8g0h6	brucella su
342	5	62.5	368	16	Q8CZW8	Q8czw8	yersinia pe

343	5	62.5	370	16	Q55938	Q55938	synechocyst
344	5	62.5	371	16	Q9CBV6	Q9cbv6	mycobacteri
345	5	62.5	373	2	Q8KUL2	Q8kul2	streptococc
346	5	62.5	373	2	Q8KY03	Q8ky03	mycobacteri
347	5	62.5	373	10	Q8GSY8	Q8gsy8	oryza sativ
348	5	62.5	373	17	Q8TU32	Q8tu32	methanosarc
349	5	62.5	374	16	Q8U8W8	Q8u8w8	agrobacteri
350	5	62.5	377	5	Q9N2Z4	Q9n2z4	caenorhabdi
351	5	62.5	377	16	Q8P9D6	Q8p9d6	xanthomonas
352	5	62.5	377	16	Q82SK1	Q82sk1	nitrosomona
353	5	62.5	378	12	Q9YMP1	Q9ymp1	lymantria d
354	5	62.5	380	16	Q8YHD6	Q8yhd6	brucella me
355	5	62.5	381	16	Q82GF6	Q82gf6	streptomyce
356	5	62.5	382	16	Q8CNK7	Q8cnk7	staphylococ
357	5	62.5	383	5	O17907	O17907	caenorhabdi
358	5	62.5	383	16	Q8UKL8	Q8ukl8	agrobacteri
359	5	62.5	383	17	Q8TZ57	Q8tz57	methanopyru
360	5	62.5	384	16	Q9A7D1	Q9a7d1	caulobacter
361	5	62.5	384	17	O52005	O52005	halobacteri
362	5	62.5	387	16	Q836G1	Q836g1	enterococcu
363	5	62.5	390	3	Q8TGE2	Q8tge2	aspergillus
364	5	62.5	391	5	O17791	O17791	caenorhabdi
365	5	62.5	393	3	Q9Y8D4	Q9y8d4	cochliobolu
366	5	62.5	394	16	Q8CPK4	Q8cpk4	staphylococ
367	5	62.5	397	16	Q89C49	Q89c49	bradyrhizob
368	5	62.5	398	2	Q9FD56	Q9fd56	streptococc
369	5	62.5	398	5	Q8MXQ8	Q8mxq8	caenorhabdi
370	5	62.5	398	16	Q97PB3	Q97pb3	streptococc
371	5	62.5	398	16	Q8DNS4	Q8dns4	streptococc
372	5	62.5	400	10	Q9LKR2	Q9lkr2	arabidopsis
373	5	62.5	402	2	Q9EVN6	Q9evn6	mycobacteri
374	5	62.5	402	5	Q9V6P0	Q9v6p0	drosophila
375	5	62.5	403	16	Q928P4	Q928p4	listeria in
376	5	62.5	405	4	Q9BU21	Q9bu21	homo sapien
377	5	62.5	408	13	Q7SYI1	Q7syi1	gallus gall
378	5	62.5	409	16	Q7V555	Q7v555	prochloroco
379	5	62.5	410	16	Q82Q03	Q82q03	streptomyce
380	5	62.5	410	16	Q82XG9	Q82xg9	nitrosomona
381	5	62.5	411	5	Q9VZY6	Q9vzy6	drosophila
382	5	62.5	411	16	Q8FHJ6	Q8fhj6	escherichia
383	5	62.5	415	17	P95903	P95903	sulfolobus
384	5	62.5	416	2	Q9RMC2	Q9rmc2	acinetobact
385	5	62.5	419	10	Q9FE91	Q9fe91	arabidopsis
386	5	62.5	419	11	Q9D9W6	Q9d9w6	mus musculu
387	5	62.5	424	5	Q95Q48	Q95q48	caenorhabdi
388	5	62.5	424	11	Q80XN5	Q80xn5	mus musculu
389	5	62.5	426	10	O49840	O49840	arabidopsis
390	5	62.5	426	10	Q8GYU1	Q8gyu1	arabidopsis
391	5	62.5	427	2	P95326	P95326	myxococcus
392	5	62.5	428	16	Q88K89	Q88k89	pseudomonas
393	5	62.5	432	16	O69672	O69672	mycobacteri
394	5	62.5	432	16	Q7TVW1	Q7tvw1	mycobacteri
395	5	62.5	432	17	Q8ZUS8	Q8zus8	pyrobaculum
396	5	62.5	433	16	Q88NR9	Q88nr9	pseudomonas
397	5	62.5	433	16	Q88FV1	Q88fv1	pseudomonas
398	5	62.5	434	16	Q9PKZ1	Q9pkz1	chlamydia m
399	5	62.5	435	16	Q8RG43	Q8rg43	fusobacteri

400	5	62.5	435	16	Q8R649	Q8r649 fusobacteri
401	5	62.5	436	16	Q87S40	Q87s40 vibrio para
402	5	62.5	436	16	Q7V293	Q7v293 prochloroco
403	5	62.5	437	16	Q8DEX6	Q8dex6 vibrio vuln
404	5	62.5	439	11	Q8CI06	Q8ci06 mus musculu
405	5	62.5	439	17	O26959	O26959 methanobact
406	5	62.5	441	13	Q7SYI0	Q7syi0 gallus gall
407	5	62.5	443	5	Q9VXW3	Q9vwx3 drosophila
408	5	62.5	443	16	Q8A266	Q8a266 bacteroides
409	5	62.5	443	16	Q829N5	Q829n5 streptomyce
410	5	62.5	443	16	Q83MB0	Q83mb0 shigella fl
411	5	62.5	444	2	Q9ZNI7	Q9zni7 pseudomonas
412	5	62.5	446	10	Q9LDI3	Q9ldi3 arabidopsis
413	5	62.5	446	16	Q82US1	Q82us1 nitrosomona
414	5	62.5	448	16	Q8KAZ8	Q8kaz8 chlorobium
415	5	62.5	452	2	Q9Z5U9	Q9z5u9 zymomonas m
416	5	62.5	452	3	Q9UVS9	Q9uvs9 aspergillus
417	5	62.5	453	2	Q9R9H3	Q9r9h3 pseudomonas
418	5	62.5	453	2	Q9KGS4	Q9kgs4 pseudomonas
419	5	62.5	453	17	Q8ZWM4	Q8zwm4 pyrobaculum
420	5	62.5	454	10	Q9MLA9	Q9mla9 arabidopsis
421	5	62.5	457	5	Q8MNS2	Q8mns2 caenorhabdi
422	5	62.5	458	16	Q8FRJ9	Q8frj9 corynebacte
423	5	62.5	462	5	Q9XXH3	Q9xxh3 caenorhabdi
424	5	62.5	462	16	Q9CMA1	Q9cma1 pasteurella
425	5	62.5	463	16	Q82RV1	Q82rv1 streptomyce
426	5	62.5	464	16	Q7VEF3	Q7vef3 prochloroco
427	5	62.5	465	16	Q935I8	Q935i8 salmonella
428	5	62.5	466	16	Q7VBP1	Q7vbp1 prochloroco
429	5	62.5	466	17	O59591	O59591 pyrococcus
430	5	62.5	467	16	Q8UIE1	Q8uiel agrobacteri
431	5	62.5	468	10	Q9FZM9	Q9fzm9 oryza sativ
432	5	62.5	469	10	Q7XKC8	Q7xkc8 oryza sativ
433	5	62.5	476	5	Q9V935	Q9v935 drosophila
434	5	62.5	478	10	Q84UY9	Q84uy9 oryza sativ
435	5	62.5	481	2	Q9ZG92	Q9zg92 pseudomonas
436	5	62.5	481	2	O05479	O05479 streptomyce
437	5	62.5	481	16	Q8PIX8	Q8pix8 xanthomonas
438	5	62.5	481	16	Q8P7K5	Q8p7k5 xanthomonas
439	5	62.5	481	17	O58675	O58675 pyrococcus
440	5	62.5	483	10	Q7XB57	Q7xb57 oryza sativ
441	5	62.5	483	16	Q8YJH4	Q8yjh4 brucella me
442	5	62.5	485	2	Q8VUS9	Q8vus9 paracoccus
443	5	62.5	486	11	Q8R584	Q8r584 mus musculu
444	5	62.5	490	16	Q9A2Z5	Q9a2z5 caulobacter
445	5	62.5	490	16	Q8EE98	Q8ee98 shewanella
446	5	62.5	493	5	Q8T8T5	Q8t8t5 drosophila
447	5	62.5	493	10	Q9LRA5	Q9lra5 arabidopsis
448	5	62.5	493	10	Q8LMT0	Q8lmt0 oryza sativ
449	5	62.5	494	17	O29412	O29412 archaeoglob
450	5	62.5	495	11	Q8BZE5	Q8bze5 mus musculu
451	5	62.5	497	5	Q18516	Q18516 caenorhabdi
452	5	62.5	499	16	Q55373	Q55373 synechocyst
453	5	62.5	500	17	O28844	O28844 archaeoglob
454	5	62.5	504	10	Q9S9Z1	Q9s9z1 arabidopsis
455	5	62.5	504	11	Q9JM73	Q9jm73 mus musculu
456	5	62.5	507	10	Q8LMJ9	Q8lmj9 oryza sativ

457	5	62.5	507	16	Q82CV0	Q82cv0 streptomyce
458	5	62.5	509	9	Q9ZX71	Q9zx71 mycobacteri
459	5	62.5	510	11	Q8CFS9	Q8cfs9 mus musculu
460	5	62.5	511	16	Q8G5R8	Q8g5r8 bifidobacte
461	5	62.5	514	2	Q8KJG3	Q8kjpg3 rhizobium l
462	5	62.5	514	16	Q98A94	Q98a94 rhizobium l
463	5	62.5	518	16	Q7V4Z0	Q7v4z0 prochloroco
464	5	62.5	524	16	Q9ADN6	Q9adn6 streptomyce
465	5	62.5	526	2	Q9RQ03	Q9rq03 xanthobacte
466	5	62.5	527	16	Q894S3	Q894s3 clostridium
467	5	62.5	530	16	Q9CIK5	Q9cik5 lactococcus
468	5	62.5	532	3	Q8NK00	Q8nk00 trichoderma
469	5	62.5	533	11	Q8BQL2	Q8bql2 mus musculu
470	5	62.5	533	16	Q98F95	Q98f95 rhizobium l
471	5	62.5	533	16	Q8FZ18	Q8fz18 brucella su
472	5	62.5	538	16	Q8YIU3	Q8yiu3 brucella me
473	5	62.5	539	4	Q9NW45	Q9nw45 homo sapien
474	5	62.5	539	4	Q9NWD6	Q9nwd6 homo sapien
475	5	62.5	541	16	Q8G3E2	Q8g3e2 brucella su
476	5	62.5	541	16	Q7VA17	Q7val7 prochloroco
477	5	62.5	545	10	Q8S9K1	Q8s9k1 arabidopsis
478	5	62.5	546	16	Q9AA45	Q9aa45 caulobacter
479	5	62.5	548	17	Q9HJZ5	Q9hjjz5 thermoplasm
480	5	62.5	550	16	Q8YEE0	Q8yee0 brucella me
481	5	62.5	554	10	Q9S9X4	Q9s9x4 arabidopsis
482	5	62.5	555	5	Q20402	Q20402 caenorhabdi
483	5	62.5	555	11	Q8CDY1	Q8cdyl mus musculu
484	5	62.5	556	4	Q96E57	Q96e57 homo sapien
485	5	62.5	556	5	O15929	O15929 plasmodium
486	5	62.5	557	13	Q90Z52	Q90z52 brachydanio
487	5	62.5	557	16	Q8D4Y0	Q8d4y0 vibrio vuln
488	5	62.5	560	16	Q8F6P3	Q8f6p3 leptospira
489	5	62.5	561	5	Q95P96	Q95p96 patinopecte
490	5	62.5	567	4	Q8N8E3	Q8n8e3 homo sapien
491	5	62.5	570	5	Q9U2R1	Q9u2r1 caenorhabdi
492	5	62.5	570	11	Q8CIH1	Q8cihl mus musculu
493	5	62.5	570	11	Q8QZX2	Q8qzx2 mus musculu
494	5	62.5	570	16	Q97IV7	Q97iv7 clostridium
495	5	62.5	571	4	Q9BSW6	Q9bsw6 homo sapien
496	5	62.5	572	5	Q9XXH4	Q9xxh4 caenorhabdi
497	5	62.5	579	4	Q9H2N2	Q9h2n2 homo sapien
498	5	62.5	579	17	Q9V1X6	Q9v1x6 pyrococcus
499	5	62.5	580	17	O59381	O59381 pyrococcus
500	5	62.5	581	16	Q9ADI5	Q9adi5 streptomyce
501	5	62.5	581	16	Q82L53	Q82l53 streptomyce
502	5	62.5	582	16	O33678	O33678 rhizobium m
503	5	62.5	586	10	Q93XM8	Q93xm8 malus domes
504	5	62.5	591	11	Q80XI7	Q80xi7 mus musculu
505	5	62.5	596	2	Q56360	Q56360 thiocapsa r
506	5	62.5	597	10	O81103	O81103 prunus arme
507	5	62.5	597	16	Q9PPX0	Q9ppx0 ureaplasma
508	5	62.5	600	5	Q9V7T7	Q9v7t7 drosophila
509	5	62.5	604	5	Q8IGT9	Q8igt9 drosophila
510	5	62.5	605	16	Q8DGW0	Q8dgw0 synechococc
511	5	62.5	607	16	Q9F2E0	Q9f2e0 salmonella
512	5	62.5	607	16	Q9F2I6	Q9f2i6 salmonella
513	5	62.5	607	16	Q8ZJR3	Q8zjr3 yersinia pe

514	5	62.5	607	16	Q83SU6	Q83su6 salmonella
515	5	62.5	608	10	Q9FFD4	Q9ffd4 arabidopsis
516	5	62.5	611	5	Q23454	Q23454 caenorhabdi
517	5	62.5	614	4	Q8WU94	Q8wu94 homo sapien
518	5	62.5	614	4	Q96SR8	Q96sr8 homo sapien
519	5	62.5	615	16	Q8UAJ0	Q8uaj0 agrobacteri
520	5	62.5	616	5	Q8IQZ8	Q8iqz8 drosophila
521	5	62.5	618	3	Q96TI3	Q96ti3 lentinula e
522	5	62.5	619	10	Q9M648	Q9m648 arabidopsis
523	5	62.5	619	10	Q9C9W9	Q9c9w9 arabidopsis
524	5	62.5	622	2	Q51862	Q51862 pseudomonas
525	5	62.5	622	16	Q823G8	Q823g8 chlamydomphi
526	5	62.5	623	17	Q8PXC9	Q8pxc9 methanosarc
527	5	62.5	625	11	Q8C6N7	Q8c6n7 mus musculu
528	5	62.5	626	10	Q9SW44	Q9sw44 arabidopsis
529	5	62.5	626	16	Q8ZCN4	Q8zcn4 yersinia pe
530	5	62.5	635	11	O55002	O55002 mus musculu
531	5	62.5	635	16	Q93IU4	Q93iu4 streptomyce
532	5	62.5	637	16	Q55413	Q55413 synechocyst
533	5	62.5	637	16	Q8EFU5	Q8efu5 shewanella
534	5	62.5	639	2	Q9AI10	Q9ai10 photorhabdu
535	5	62.5	640	5	O61604	O61604 drosophila
536	5	62.5	640	5	Q9NAP5	Q9nap5 caenorhabdi
537	5	62.5	641	5	Q8IQZ7	Q8iqz7 drosophila
538	5	62.5	644	12	Q90063	Q90063 nudaurelia
539	5	62.5	646	5	Q25017	Q25017 helix asper
540	5	62.5	650	10	Q9SGR9	Q9sgr9 arabidopsis
541	5	62.5	657	11	Q8CGJ9	Q8cgj9 mus musculu
542	5	62.5	658	11	Q8BFS4	Q8bfs4 mus musculu
543	5	62.5	663	11	O70434	O70434 mus musculu
544	5	62.5	668	10	Q9LSS0	Q9lss0 arabidopsis
545	5	62.5	672	10	Q9ZWB1	Q9zwb1 arabidopsis
546	5	62.5	672	10	Q851R1	Q851r1 oryza sativ
547	5	62.5	673	4	Q8IWK1	Q8iwl1 homo sapien
548	5	62.5	680	11	O55001	O55001 mus musculu
549	5	62.5	680	16	Q89UJ2	Q89uj2 bradyrhizob
550	5	62.5	686	16	Q92QA5	Q92qa5 rhizobium m
551	5	62.5	691	10	Q9FHX3	Q9fhx3 arabidopsis
552	5	62.5	694	16	Q8A3X0	Q8a3x0 bacteroides
553	5	62.5	695	8	Q8HSD0	Q8hsd0 solanum hav
554	5	62.5	697	11	Q8K4V6	Q8k4v6 mus musculu
555	5	62.5	697	16	Q8EB65	Q8eb65 shewanella
556	5	62.5	698	5	Q7YU82	Q7yu82 drosophila
557	5	62.5	705	5	Q7YY00	Q7yy00 cryptospori
558	5	62.5	709	16	Q8P6C0	Q8p6c0 xanthomonas
559	5	62.5	713	16	Q8PHS3	Q8phs3 xanthomonas
560	5	62.5	714	16	Q97FP1	Q97fp1 clostridium
561	5	62.5	716	10	Q8H8C1	Q8h8c1 oryza sativ
562	5	62.5	718	10	Q93ZR5	Q93zr5 arabidopsis
563	5	62.5	718	10	Q9LSR8	Q9lsr8 arabidopsis
564	5	62.5	719	5	Q9VM92	Q9vm92 drosophila
565	5	62.5	725	5	Q86J51	Q86j51 dictyosteli
566	5	62.5	726	2	Q9LAE4	Q9lae4 azospirillu
567	5	62.5	726	10	Q7Y1Z5	Q7ylz5 arabidopsis
568	5	62.5	738	5	O15646	O15646 dictyosteli
569	5	62.5	738	5	Q86IQ2	Q86iq2 dictyosteli
570	5	62.5	742	2	O68598	O68598 pseudomonas

571	5	62.5	742	12	Q9Wau9	Q9wau9 broad bean
572	5	62.5	742	12	Q9Wau7	Q9wau7 broad bean
573	5	62.5	742	12	Q9Wau8	Q9wau8 broad bean
574	5	62.5	742	16	Q9I527	Q9i527 pseudomonas
575	5	62.5	742	16	Q8EUW3	Q8euw3 mycoplasma
576	5	62.5	749	10	Q9LE23	Q9le23 oryza sativ
577	5	62.5	753	16	Q8Y5E3	Q8y5e3 listeria mo
578	5	62.5	757	10	Q8RXQ7	Q8rxq7 arabidopsis
579	5	62.5	763	16	Q8FMM3	Q8fmm3 corynebacte
580	5	62.5	768	10	Q9LHU0	Q9lhu0 oryza sativ
581	5	62.5	770	16	Q8U9Q3	Q8u9q3 agrobacteri
582	5	62.5	771	13	Q9I8K4	Q9i8k4 rana catesb
583	5	62.5	771	16	Q89N45	Q89n45 bradyrhizob
584	5	62.5	772	5	Q8IJD2	Q8ijd2 plasmodium
585	5	62.5	779	3	O14325	O14325 schizosacch
586	5	62.5	780	10	Q9MA68	Q9ma68 arabidopsis
587	5	62.5	780	16	Q8PI15	Q8pi15 xanthomonas
588	5	62.5	781	16	Q8P6S1	Q8p6s1 xanthomonas
589	5	62.5	782	5	Q8WQC0	Q8wqc0 caenorhabdi
590	5	62.5	783	3	O14130	O14130 schizosacch
591	5	62.5	784	16	Q8PN94	Q8pn94 xanthomonas
592	5	62.5	788	16	Q8DR28	Q8dr28 streptococc
593	5	62.5	789	2	Q9F599	Q9f599 agrobacteri
594	5	62.5	790	16	Q9PF36	Q9pf36 xylella fas
595	5	62.5	790	16	Q9KS24	Q9ks24 vibrio chol
596	5	62.5	790	16	Q87AJ3	Q87aj3 xylella fas
597	5	62.5	791	10	Q94HY0	Q94hy0 oryza sativ
598	5	62.5	791	10	Q7XCS1	Q7xcs1 oryza sativ
599	5	62.5	793	12	Q64787	Q64787 avian adeno
600	5	62.5	796	16	Q9Z4W5	Q9z4w5 streptomyce
601	5	62.5	799	13	Q7SYH9	Q7syh9 gallus gall
602	5	62.5	803	5	Q8IBJ5	Q8ibj5 plasmodium
603	5	62.5	805	5	Q8MLR1	Q8mlr1 drosophila
604	5	62.5	808	10	Q9LNV7	Q9lnv7 arabidopsis
605	5	62.5	815	16	Q9CPD4	Q9cpd4 pasteurella
606	5	62.5	819	5	Q95Q49	Q95q49 caenorhabdi
607	5	62.5	819	16	Q8ZIN6	Q8zin6 yersinia pe
608	5	62.5	823	10	Q9MA70	Q9ma70 arabidopsis
609	5	62.5	824	3	Q9Y7F1	Q9y7f1 aspergillus
610	5	62.5	824	12	O12663	O12663 broad bean
611	5	62.5	827	3	O43051	O43051 schizosacch
612	5	62.5	837	5	O62329	O62329 caenorhabdi
613	5	62.5	841	11	Q8R2Z1	Q8r2z1 mus musculu
614	5	62.5	841	11	O54999	O54999 mus musculu
615	5	62.5	841	11	P97484	P97484 mus musculu
616	5	62.5	841	16	Q83HB7	Q83hb7 tropheryma
617	5	62.5	841	16	Q83FM2	Q83fm2 tropheryma
618	5	62.5	843	5	O02264	O02264 caenorhabdi
619	5	62.5	845	5	Q8WPP8	Q8wpp8 trypanosoma
620	5	62.5	845	16	Q8CZP2	Q8czp2 yersinia pe
621	5	62.5	846	16	Q9PN76	Q9pn76 campylobact
622	5	62.5	847	16	Q8EEC3	Q8eec3 shewanella
623	5	62.5	849	10	Q9SHG6	Q9shg6 arabidopsis
624	5	62.5	853	11	Q8C0R9	Q8c0r9 mus musculu
625	5	62.5	860	5	Q9NAB5	Q9nab5 caenorhabdi
626	5	62.5	863	16	Q7U078	Q7u078 mycobacteri
627	5	62.5	866	5	Q9VF20	Q9vf20 drosophila

628	5	62.5	870	5	P91346	P91346 caenorhabdi
629	5	62.5	874	2	Q9S3L0	Q9s3l0 clostridium
630	5	62.5	877	16	O86365	O86365 mycobacteri
631	5	62.5	877	16	Q7U1Q1	Q7u1q1 mycobacteri
632	5	62.5	882	11	Q9R206	Q9r206 mus musculu
633	5	62.5	882	11	O70353	O70353 mus musculu
634	5	62.5	884	6	O97583	O97583 bos taurus
635	5	62.5	884	16	Q8P5B4	Q8p5b4 xanthomonas
636	5	62.5	885	16	Q8PPJ3	Q8ppj3 xanthomonas
637	5	62.5	886	3	Q875Q0	Q875q0 saccharomyc
638	5	62.5	894	10	Q8VYW8	Q8vyw8 arabidopsis
639	5	62.5	898	5	Q8SV30	Q8sv30 encephalito
640	5	62.5	904	5	Q8MLR0	Q8mlr0 drosophila
641	5	62.5	908	10	Q7XXE6	Q7xxe6 oryza sativ
642	5	62.5	911	4	Q7Z7D0	Q7z7d0 homo sapien
643	5	62.5	914	5	Q9W1L9	Q9w1l9 drosophila
644	5	62.5	915	16	Q8EUK1	Q8euk1 mycoplasma
645	5	62.5	917	3	Q8X032	Q8x032 neurospora
646	5	62.5	917	4	Q8NFN4	Q8nfn4 homo sapien
647	5	62.5	917	4	Q8WXA0	Q8wxa0 homo sapien
648	5	62.5	917	4	Q8IUQ1	Q8iuq1 homo sapien
649	5	62.5	922	16	Q89ST3	Q89st3 bradyrhizob
650	5	62.5	930	11	Q925G9	Q925g9 mus musculu
651	5	62.5	931	16	Q8RD56	Q8rd56 thermoanaer
652	5	62.5	933	5	P91129	P91129 caenorhabdi
653	5	62.5	937	12	Q9Q2Q2	Q9q2q2 broad bean
654	5	62.5	937	12	Q9WDH0	Q9wdh0 broad bean
655	5	62.5	955	5	Q19945	Q19945 caenorhabdi
656	5	62.5	956	16	Q7WDA9	Q7wda9 bordetella
657	5	62.5	956	16	Q7VZ18	Q7vz18 bordetella
658	5	62.5	957	16	Q7W5S2	Q7w5s2 bordetella
659	5	62.5	967	11	Q920Q9	Q920q9 rattus norv
660	5	62.5	969	17	Q8U1U6	Q8ulu6 pyrococcus
661	5	62.5	976	16	Q9AB92	Q9ab92 caulobacter
662	5	62.5	985	2	P94324	P94324 bradyrhizob
663	5	62.5	985	16	Q89X63	Q89x63 bradyrhizob
664	5	62.5	989	2	Q8KTI7	Q8kti7 methylobact
665	5	62.5	991	11	Q8C0M0	Q8c0m0 mus musculu
666	5	62.5	997	5	Q967Z1	Q967z1 trypanosoma
667	5	62.5	1001	10	Q8LSP2	Q8lsp2 oryza sativ
668	5	62.5	1002	10	Q9ARQ7	Q9arq7 oryza sativ
669	5	62.5	1008	16	Q9PEJ2	Q9pej2 xylella fas
670	5	62.5	1008	16	Q87EI9	Q87ei9 xylella fas
671	5	62.5	1013	17	Q97C94	Q97c94 thermoplasm
672	5	62.5	1017	5	Q8IPL3	Q8ipl3 drosophila
673	5	62.5	1017	10	Q9LKV5	Q9lkv5 arabidopsis
674	5	62.5	1042	5	Q9W4W2	Q9w4w2 drosophila
675	5	62.5	1042	5	O76911	O76911 drosophila
676	5	62.5	1042	5	Q9UB20	Q9ub20 drosophila
677	5	62.5	1042	16	Q97G63	Q97g63 clostridium
678	5	62.5	1047	10	Q9FY54	Q9fy54 arabidopsis
679	5	62.5	1053	11	Q80YP5	Q80yp5 mus musculu
680	5	62.5	1055	3	Q9C1J9	Q9c1j9 cryptococcu
681	5	62.5	1064	12	Q9IR41	Q9ir41 broad bean
682	5	62.5	1064	12	Q9YM09	Q9ym09 broad bean
683	5	62.5	1064	12	Q9WAU6	Q9wau6 broad bean
684	5	62.5	1064	12	Q9IZU4	Q9izu4 broad bean

685	5	62.5	1064	12	Q9Z006	Q9z006 patchouli m
686	5	62.5	1065	12	Q9Q2Q3	Q9q2q3 broad bean
687	5	62.5	1072	16	Q98LC1	Q98lc1 rhizobium l
688	5	62.5	1093	4	Q8NFN5	Q8nfn5 homo sapien
689	5	62.5	1100	10	Q9M319	Q9m319 arabidopsis
690	5	62.5	1105	11	Q8BMJ4	Q8bmj4 mus musculu
691	5	62.5	1115	4	O75189	O75189 homo sapien
692	5	62.5	1115	5	O17267	O17267 caenorhabdi
693	5	62.5	1130	5	Q8ITY8	Q8ity8 caenorhabdi
694	5	62.5	1136	16	Q88SK2	Q88sk2 lactobacill
695	5	62.5	1140	15	Q8J6D9	Q8j6d9 simian foam
696	5	62.5	1143	15	O12817	O12817 human spuma
697	5	62.5	1146	15	Q87040	Q87040 simian foam
698	5	62.5	1169	11	Q9QXH4	Q9qXH4 mus musculu
699	5	62.5	1178	16	Q7ZAL0	Q7zal0 streptococc
700	5	62.5	1179	16	Q97QG7	Q97qg7 streptococc
701	5	62.5	1181	5	Q9VBP3	Q9vbp3 drosophila
702	5	62.5	1181	5	Q9XZ37	Q9xz37 drosophila
703	5	62.5	1198	4	Q8IVE1	Q8ive1 homo sapien
704	5	62.5	1200	11	Q8BGF7	Q8bgf7 mus musculu
705	5	62.5	1210	10	Q93ZM5	Q93zm5 arabidopsis
706	5	62.5	1241	5	Q9W3L1	Q9w3l1 drosophila
707	5	62.5	1243	16	Q9RDG5	Q9rdg5 streptomyce
708	5	62.5	1249	16	Q8REU9	Q8reu9 fusobacteri
709	5	62.5	1251	10	Q9MA34	Q9ma34 arabidopsis
710	5	62.5	1257	16	Q82CP4	Q82cp4 streptomyce
711	5	62.5	1275	17	Q8Q061	Q8q061 methanosarc
712	5	62.5	1292	16	Q87LC6	Q87lc6 vibrio para
713	5	62.5	1301	12	Q91LK4	Q91lk4 white spot
714	5	62.5	1301	12	Q918H8	Q918h8 white spot
715	5	62.5	1301	16	Q89W28	Q89w28 bradyrhizob
716	5	62.5	1324	16	Q82VX1	Q82vx1 nitrosomona
717	5	62.5	1327	4	Q9Y2L2	Q9y2l2 homo sapien
718	5	62.5	1330	2	Q55284	Q55284 synechocyst
719	5	62.5	1365	2	Q8KWD2	Q8kwd2 ruegeria sp
720	5	62.5	1386	5	Q9GRS8	Q9grs8 leishmania
721	5	62.5	1399	5	Q9V4R0	Q9v4r0 drosophila
722	5	62.5	1449	5	Q8T675	Q8t675 dictyosteli
723	5	62.5	1523	4	Q7Z3K4	Q7z3k4 homo sapien
724	5	62.5	1527	5	Q8I425	Q8i425 plasmodium
725	5	62.5	1527	16	Q7V505	Q7v505 prochloroco
726	5	62.5	1529	5	Q9W4Y9	Q9w4y9 drosophila
727	5	62.5	1566	5	Q9XUF9	Q9xuf9 caenorhabdi
728	5	62.5	1569	16	Q88KK3	Q88kk3 pseudomonas
729	5	62.5	1623	5	Q9U3U7	Q9u3u7 anopheles g
730	5	62.5	1724	5	Q9N583	Q9n583 caenorhabdi
731	5	62.5	1758	5	Q95Y84	Q95y84 caenorhabdi
732	5	62.5	1773	5	Q8WPD8	Q8wpd8 ciona intes
733	5	62.5	1815	16	Q92VA6	Q92va6 rhizobium m
734	5	62.5	1852	3	O13281	O13281 emericella
735	5	62.5	1857	3	Q8TGC5	Q8tgc5 aspergillus
736	5	62.5	1932	16	Q7UQ94	Q7uq94 rhodopirell
737	5	62.5	2028	8	Q32064	Q32064 chlamydomon
738	5	62.5	2102	5	Q86IW7	Q86iw7 d similar t
739	5	62.5	2190	12	Q915A5	Q915a5 pichinde ar
740	5	62.5	2195	12	Q8VAB2	Q8vab2 white spot
741	5	62.5	2351	12	Q91LL2	Q91ll2 white spot

742	5	62.5	2351	12	Q8QTG5	Q8qtg5 white spot
743	5	62.5	2364	2	Q46342	Q46342 clostridium
744	5	62.5	2367	10	Q7X970	Q7x970 oryza sativ
745	5	62.5	2413	2	Q9FDB0	Q9fdb0 vibrio chol
746	5	62.5	2588	11	O88491	O88491 mus musculu
747	5	62.5	2701	4	Q9Y520	Q9y520 homo sapien
748	5	62.5	2756	2	O33904	O33904 shewanella
749	5	62.5	2849	9	Q8W6K4	Q8w6k4 sinorhizobi
750	5	62.5	3063	2	Q59497	Q59497 corynebacte
751	5	62.5	3522	5	Q86NF7	Q86nf7 caenorhabdi
752	5	62.5	3563	5	Q95NZ2	Q95nz2 caenorhabdi
753	5	62.5	3600	10	Q9SA64	Q9sa64 arabidopsis
754	5	62.5	3685	4	Q14205	Q14205 homo sapien
755	5	62.5	3848	2	P94772	P94772 erwinia chr
756	5	62.5	4342	16	Q9I157	Q9i157 pseudomonas
757	5	62.5	4488	11	Q9QZH1	Q9qzh1 mus musculu
758	5	62.5	4559	5	Q9U3Y5	Q9u3y5 drosophila
759	5	62.5	4666	10	Q7XQ92	Q7xq92 oryza sativ
760	5	62.5	4730	5	Q8T128	Q8t128 dictyosteli
761	5	62.5	4801	2	Q9AIT3	Q9ait3 xanthomonas
762	5	62.5	4918	5	Q867N2	Q867n2 caenorhabdi
763	5	62.5	4929	5	Q867D9	Q867d9 caenorhabdi
764	5	62.5	4944	5	Q86NG0	Q86ng0 caenorhabdi
765	5	62.5	8601	2	Q8GM87	Q8gm87 symbiont ba
766	5	62.5	9477	2	Q9L4X3	Q9l4x3 streptomyce
767	5	62.5	9510	2	Q93NX9	Q93nx9 streptomyce
768	5	62.5	20925	3	Q8NJX1	Q8njx1 trichoderma
769	4	50.0	9	2	P72149	P72149 pseudomonas
770	4	50.0	17	2	P83329	P83329 streptococc
771	4	50.0	17	11	Q61932	Q61932 mus musculu
772	4	50.0	19	4	Q9UCC8	Q9ucc8 homo sapien
773	4	50.0	20	2	Q9R4E9	Q9r4e9 rhodopseudo
774	4	50.0	26	5	Q9BM03	Q9bm03 dugesia tig
775	4	50.0	26	7	O46850	O46850 triakis scy
776	4	50.0	28	4	Q9UCD1	Q9ucd1 homo sapien
777	4	50.0	30	4	Q9UCA9	Q9uca9 homo sapien
778	4	50.0	30	11	Q9QV42	Q9qv42 rattus sp.
779	4	50.0	32	2	Q9R5Q7	Q9r5q7 aeromonas h
780	4	50.0	33	4	Q9UC33	Q9uc33 homo sapien
781	4	50.0	33	5	Q9GTB2	Q9gtb2 eimeria ten
782	4	50.0	33	5	Q9GTC2	Q9gtc2 plasmodium
783	4	50.0	33	5	Q9GTA9	Q9gta9 sarcocystis
784	4	50.0	33	5	Q9GT95	Q9gt95 cryptospori
785	4	50.0	33	5	Q9GTA2	Q9gta2 babesia bov
786	4	50.0	33	12	O89876	O89876 budgerigar
787	4	50.0	33	12	O89877	O89877 budgerigar
788	4	50.0	33	12	O89886	O89886 budgerigar
789	4	50.0	33	12	O89885	O89885 budgerigar
790	4	50.0	33	12	O89871	O89871 budgerigar
791	4	50.0	33	12	O89881	O89881 budgerigar
792	4	50.0	33	12	O89874	O89874 budgerigar
793	4	50.0	33	12	O89884	O89884 budgerigar
794	4	50.0	33	12	O89882	O89882 budgerigar
795	4	50.0	33	12	O89873	O89873 budgerigar
796	4	50.0	33	12	O89883	O89883 budgerigar
797	4	50.0	33	12	O89879	O89879 budgerigar
798	4	50.0	33	12	O89875	O89875 budgerigar

799	4	50.0	33	12	O89872	O89872 budgerigar
800	4	50.0	33	12	O89887	O89887 budgerigar
801	4	50.0	33	12	O89880	O89880 budgerigar
802	4	50.0	33	12	O89878	O89878 budgerigar
803	4	50.0	33	16	Q9PH79	Q9ph79 xylella fas
804	4	50.0	33	16	Q97RJ3	Q97rj3 streptococc
805	4	50.0	33	16	Q7VFH8	Q7vfh8 helicobacte
806	4	50.0	35	4	Q8WZ99	Q8wz99 homo sapien
807	4	50.0	36	16	Q8VJK4	Q8vjk4 mycobacteri
808	4	50.0	36	16	Q83D85	Q83d85 coxiella bu
809	4	50.0	39	2	Q9R891	Q9r891 chlamydia t
810	4	50.0	40	2	O68327	O68327 caulobacter
811	4	50.0	40	16	Q8ECU5	Q8ecu5 shewanella
812	4	50.0	41	2	Q9RZX2	Q9rzx2 borrelia bu
813	4	50.0	41	6	Q9N194	Q9n194 macaca mula
814	4	50.0	41	6	Q9N191	Q9n191 hylobates l
815	4	50.0	41	6	Q9N193	Q9n193 gorilla gor
816	4	50.0	41	6	Q9N192	Q9n192 pan troglod
817	4	50.0	41	16	Q8PGA4	Q8pga4 xanthomonas
818	4	50.0	41	16	Q8F414	Q8f414 leptospira
819	4	50.0	42	2	Q53299	Q53299 escherichia
820	4	50.0	42	12	Q9YPJ0	Q9ypj0 avian infec
821	4	50.0	42	15	Q9Q582	Q9q582 human immun
822	4	50.0	44	2	Q47324	Q47324 escherichia
823	4	50.0	44	16	Q99QL7	Q99ql7 streptomyce
824	4	50.0	44	16	Q8E9C1	Q8e9c1 shewanella
825	4	50.0	44	16	Q8DAR5	Q8dar5 vibrio vuln
826	4	50.0	44	16	Q7UQP3	Q7uqp3 rhodopirell
827	4	50.0	45	4	Q9HCW4	Q9hcw4 homo sapien
828	4	50.0	46	16	Q9A039	Q9a039 streptococc
829	4	50.0	47	10	Q7XS03	Q7xs03 oryza sativ
830	4	50.0	48	12	Q85243	Q85243 potato viru
831	4	50.0	49	7	Q9GIQ2	Q9giq2 eschrichtiu
832	4	50.0	49	16	Q8KF81	Q8kf81 chlorobium
833	4	50.0	50	5	Q8T642	Q8t642 ceratitidis c
834	4	50.0	50	5	Q8T643	Q8t643 ceratitidis c
835	4	50.0	50	12	Q91FI6	Q91fi6 chilo iride
836	4	50.0	50	12	Q85239	Q85239 potato viru
837	4	50.0	50	13	Q08135	Q08135 pseudopleur
838	4	50.0	50	16	Q8X453	Q8x453 escherichia
839	4	50.0	50	16	Q8FF68	Q8ff68 escherichia
840	4	50.0	51	2	Q51106	Q51106 neisseria m
841	4	50.0	51	2	Q9F8M3	Q9f8m3 carboxydoth
842	4	50.0	51	5	Q26905	Q26905 trichostron
843	4	50.0	51	16	Q8RAW6	Q8raw6 thermoanaer
844	4	50.0	51	16	Q8G1Q7	Q8glq7 brucella su
845	4	50.0	51	16	Q8FVK0	Q8fvk0 brucella su
846	4	50.0	52	7	Q9XR67	Q9xr67 oncorhynch
847	4	50.0	52	7	Q9XR64	Q9xr64 oncorhynch
848	4	50.0	52	7	Q9XR66	Q9xr66 oncorhynch
849	4	50.0	52	7	Q9XR65	Q9xr65 oncorhynch
850	4	50.0	53	16	Q89T69	Q89t69 bradyrhizob
851	4	50.0	53	16	Q81TE4	Q81te4 bacillus an
852	4	50.0	53	16	Q81G86	Q81g86 bacillus ce
853	4	50.0	53	16	Q7UMV1	Q7umv1 rhodopirell
854	4	50.0	54	16	Q99ZY5	Q99zy5 streptococc
855	4	50.0	54	16	Q8DTS1	Q8dts1 streptococc

856	4	50.0	55	2	Q9XC71	Q9xc71 salmonella
857	4	50.0	55	10	Q38994	Q38994 arabidopsis
858	4	50.0	57	2	Q8RIW6	Q8riw6 streptococc
859	4	50.0	57	7	Q29998	Q29998 homo sapien
860	4	50.0	57	7	Q29997	Q29997 homo sapien
861	4	50.0	57	10	Q38993	Q38993 arabidopsis
862	4	50.0	57	12	Q91TH0	Q91th0 tupaia herp
863	4	50.0	58	17	Q977A3	Q977a3 sulfolobus
864	4	50.0	59	9	Q855I4	Q855i4 mycobacteri
865	4	50.0	59	10	Q8GRR3	Q8grr3 oryza sativ
866	4	50.0	60	16	Q8FUJ6	Q8fuj6 corynebacte
867	4	50.0	61	2	Q56859	Q56859 yersinia en
868	4	50.0	61	3	Q9UTY5	Q9uty5 schizosacch
869	4	50.0	61	9	Q857Y1	Q857y1 mycobacteri
870	4	50.0	61	16	Q9KPP8	Q9kpp8 vibrio chol
871	4	50.0	62	5	Q8MUB1	Q8mub1 mesobuthus
872	4	50.0	62	5	Q7YVW6	Q7yvw6 trypanosoma
873	4	50.0	62	5	Q7YSI4	Q7ysi4 trypanosoma
874	4	50.0	62	10	Q9XF78	Q9xf78 oryza sativ
875	4	50.0	62	10	Q39072	Q39072 arabidopsis
876	4	50.0	62	16	Q8NPR0	Q8npr0 corynebacte
877	4	50.0	62	16	Q7WKU6	Q7wku6 bordetella
878	4	50.0	62	16	Q7W7F8	Q7w7f8 bordetella
879	4	50.0	62	16	Q7VVB1	Q7vvb1 bordetella
880	4	50.0	63	2	Q9RP37	Q9rp37 mycobacteri
881	4	50.0	63	2	Q93PX9	Q93px9 pseudomonas
882	4	50.0	63	17	Q8ZY13	Q8zyl13 pyrobaculum
883	4	50.0	64	2	Q8KK86	Q8kk86 proteus vul
884	4	50.0	64	9	Q8HAG9	Q8hag9 salmonella
885	4	50.0	65	8	Q85MU1	Q85mul homo sapien
886	4	50.0	65	16	Q8YGX3	Q8ygx3 brucella me
887	4	50.0	65	16	Q81Q04	Q81q04 bacillus an
888	4	50.0	66	2	P97017	P97017 aeromonas j
889	4	50.0	66	10	Q7XNZ4	Q7xnz4 oryza sativ
890	4	50.0	66	12	Q8QIA7	Q8qia7 hepatitis c
891	4	50.0	66	12	Q84302	Q84302 human papil
892	4	50.0	66	12	Q80DG6	Q80dg6 hepatitis c
893	4	50.0	66	12	Q80D76	Q80d76 hepatitis c
894	4	50.0	66	16	Q92ZR2	Q92zr2 rhizobium m
895	4	50.0	66	16	Q8YJG6	Q8yjpg6 brucella me
896	4	50.0	66	16	O50486	O50486 streptomyce
897	4	50.0	66	16	Q8G0Y9	Q8g0y9 brucella su
898	4	50.0	67	2	Q9L8X0	Q9l8x0 streptomyce
899	4	50.0	67	2	Q9L8X2	Q9l8x2 streptomyce
900	4	50.0	67	10	Q8L9S8	Q8l9s8 arabidopsis
901	4	50.0	67	16	Q8XBH8	Q8xbh8 escherichia
902	4	50.0	67	16	Q7UGP7	Q7ugp7 rhodopirell
903	4	50.0	68	2	Q52624	Q52624 proteus vul
904	4	50.0	68	5	Q9TXY3	Q9txy3 caenorhabdi
905	4	50.0	68	5	Q9BL96	Q9bl96 caenorhabdi
906	4	50.0	68	16	Q9KN04	Q9kn04 vibrio chol
907	4	50.0	68	16	Q8R6R7	Q8r6r7 thermoanaer
908	4	50.0	69	12	Q8VAI7	Q8vai7 white spot
909	4	50.0	69	16	Q8XPH7	Q8xph7 ralstonia s
910	4	50.0	69	16	Q8DFY4	Q8dfy4 vibrio vuln
911	4	50.0	69	16	Q88KL5	Q88kl5 pseudomonas
912	4	50.0	70	12	Q85247	Q85247 potato viru

913	4	50.0	70	12	Q98622	Q98622 potato viru
914	4	50.0	70	16	Q8PJ81	Q8pj81 xanthomonas
915	4	50.0	70	16	Q83FD3	Q83fd3 coxiella bu
916	4	50.0	70	17	Q8PT31	Q8pt31 methanosarc
917	4	50.0	71	2	Q9ZN67	Q9zn67 ruminobacte
918	4	50.0	71	2	Q93PT2	Q93pt2 lactococcus
919	4	50.0	71	9	Q854I4	Q854i4 mycobacteri
920	4	50.0	71	16	Q8A4Q1	Q8a4q1 bacteroides
921	4	50.0	72	5	Q8IDT7	Q8idt7 plasmodium
922	4	50.0	72	9	Q8HA64	Q8ha64 bacterioph
923	4	50.0	72	9	Q8HA55	Q8ha55 bacterioph
924	4	50.0	72	9	Q855R4	Q855r4 mycobacteri
925	4	50.0	72	9	Q855G5	Q855g5 mycobacteri
926	4	50.0	72	12	Q9YMU8	Q9ymu8 lymantria d
927	4	50.0	72	16	Q99TW2	Q99tw2 staphylococ
928	4	50.0	72	16	Q8NWD2	Q8nwd2 staphylococ
929	4	50.0	72	16	Q8K7S9	Q8k7s9 streptococc
930	4	50.0	73	4	O95641	O95641 homo sapien
931	4	50.0	73	9	Q855W3	Q855w3 mycobacteri
932	4	50.0	73	10	Q8GX82	Q8gx82 arabidopsis
933	4	50.0	73	16	Q8U8E9	Q8u8e9 agrobacteri
934	4	50.0	73	16	Q8X2G0	Q8x2g0 escherichia
935	4	50.0	74	2	Q9S460	Q9s460 streptococc
936	4	50.0	74	2	Q83WF4	Q83wf4 micromonosp
937	4	50.0	74	16	Q92A64	Q92a64 listeria in
938	4	50.0	74	16	Q8Y5W1	Q8y5w1 listeria mo
939	4	50.0	74	16	Q8XGR2	Q8xgr2 salmonella
940	4	50.0	74	16	Q82RD7	Q82rd7 streptomyce
941	4	50.0	74	16	Q83RL2	Q83rl2 shigella fl
942	4	50.0	75	2	Q9F4H3	Q9f4h3 yersinia en
943	4	50.0	75	2	Q48678	Q48678 lactococcus
944	4	50.0	75	6	P79246	P79246 sus scrofa
945	4	50.0	75	6	Q9GMH0	Q9gmh0 macaca mula
946	4	50.0	75	9	Q38648	Q38648 bacterioph
947	4	50.0	75	16	Q9PND7	Q9pnd7 campylobact
948	4	50.0	75	16	Q98PE6	Q98pe6 mycoplasma
949	4	50.0	75	16	Q8XVB9	Q8xvb9 ralstonia s
950	4	50.0	75	16	Q8EAN1	Q8ean1 shewanella
951	4	50.0	75	16	Q87UB3	Q87ub3 pseudomonas
952	4	50.0	75	17	Q8Q085	Q8q085 methanosarc
953	4	50.0	76	2	Q9AH64	Q9ah64 neisseria g
954	4	50.0	76	5	O02324	O02324 caenorhabdi
955	4	50.0	76	9	Q38628	Q38628 bacterioph
956	4	50.0	76	9	Q38626	Q38626 bacterioph
957	4	50.0	76	11	Q8K3X8	Q8k3x8 rattus norv
958	4	50.0	76	11	Q91Y43	Q91y43 rattus norv
959	4	50.0	76	12	Q9Q8W0	Q9q8w0 shope fibro
960	4	50.0	77	2	Q9Z3X0	Q9z3x0 sphingomona
961	4	50.0	77	11	Q99M09	Q99m09 mus musculu
962	4	50.0	77	16	Q8D8U0	Q8d8u0 vibrio vuln
963	4	50.0	77	16	Q87QH5	Q87qh5 vibrio para
964	4	50.0	77	17	O26981	O26981 methanobact
965	4	50.0	78	5	Q9NFF6	Q9nff6 plasmodium
966	4	50.0	78	16	Q8VJD0	Q8vjd0 mycobacteri
967	4	50.0	78	17	Q8TIK3	Q8tik3 methanosarc
968	4	50.0	79	11	O35463	O35463 cricetulus
969	4	50.0	79	12	Q84524	Q84524 paramecium

970	4	50.0	80	2	O85975	O85975 sphingomona
971	4	50.0	80	5	Q8T640	Q8t640 apis mellif
972	4	50.0	80	5	Q8I5N0	Q8i5n0 plasmodium
973	4	50.0	80	10	Q8L7F0	Q8l7f0 arabidopsis
974	4	50.0	80	16	Q99SP0	Q99sp0 staphylococ
975	4	50.0	80	16	Q92KC9	Q92kc9 rhizobium m
976	4	50.0	80	16	Q82VB4	Q82vb4 nitrosomona
977	4	50.0	81	2	Q83WU3	Q83wu3 thiocapsa r
978	4	50.0	81	2	Q9LA36	Q9la36 shigella dy
979	4	50.0	81	2	Q9EU23	Q9eu23 escherichia
980	4	50.0	81	4	Q9P1F3	Q9p1f3 homo sapien
981	4	50.0	81	9	Q8HAI0	Q8hai0 salmonella
982	4	50.0	81	9	Q852W3	Q852w3 mycobacteri
983	4	50.0	81	16	Q7U5U9	Q7u5u9 synechococc
984	4	50.0	82	4	Q16020	Q16020 homo sapien
985	4	50.0	82	4	Q16014	Q16014 homo sapien
986	4	50.0	82	4	Q16019	Q16019 homo sapien
987	4	50.0	82	7	Q9XRU0	Q9xru0 rattus fusc
988	4	50.0	82	7	Q9XRT7	Q9xrt7 rattus fusc
989	4	50.0	82	7	Q30582	Q30582 macaca fasc
990	4	50.0	82	7	Q30695	Q30695 macaca mula
991	4	50.0	82	7	Q30884	Q30884 papio hamad
992	4	50.0	82	7	Q30581	Q30581 macaca fasc
993	4	50.0	82	9	Q7Y3B9	Q7y3b9 stx1 conver
994	4	50.0	82	9	Q7Y2V8	Q7y2v8 stx2 conver
995	4	50.0	82	15	O90069	O90069 human immun
996	4	50.0	82	16	Q8UDZ3	Q8udz3 agrobacteri
997	4	50.0	82	16	Q8ZEE2	Q8zee2 yersinia pe
998	4	50.0	82	16	Q87P24	Q87p24 vibrio para
999	4	50.0	82	16	Q7VQG0	Q7vqg0 candidatus
1000	4	50.0	82	16	Q7V5R5	Q7v5r5 prochloroco

ALIGNMENTS

RESULT 1

Q8P193

ID Q8P193 PRELIMINARY; PRT; 54 AA.

AC Q8P193;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

DE Hypothetical protein spyM18_1000.

GN SPYM18_1000.

OS Streptococcus pyogenes (serotype M18).

OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

OC Streptococcus.

OX NCBI_TaxID=186103;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=MGAS8232 / Serotype M18;

RX MEDLINE=21927593; PubMed=11917108;

RA Smoot J.C., Barbian K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,

RA Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,

RA Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,

RA Kapur V., Daly J.A., Veasy L.G., Musser J.M.;

RT "Genome sequence and comparative microarray analysis of serotype M18
 RT group A Streptococcus strains associated with acute rheumatic fever
 RT outbreaks.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).
 DR EMBL; AE010028; AAL97638.1; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 54 AA; 6370 MW; 5ED4FECC6149C98E CRC64;

Query Match 75.0%; Score 6; DB 16; Length 54;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDA 6
 |||||
 Db 18 EVNLDA 23

RESULT 2

Q89LY8

ID Q89LY8 PRELIMINARY; PRT; 91 AA.
 AC Q89LY8;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Bsl4405 protein.
 GN BSL4405.
 OS Bradyrhizobium japonicum.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Bradyrhizobiaceae; Bradyrhizobium.
 OX NCBI_TaxID=375;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=USDA 110;
 RX MEDLINE=22484998; PubMed=12597275;
 RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
 RA Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
 RA Kohara M., Matsumoto M., Shimpō S., Tsuruoka H., Wada T., Yamada M.,
 RA Tabata S.;
 RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
 RT Bradyrhizobium japonicum USDA110.";
 RL DNA Res. 9:189-197(2002).
 DR EMBL; AP005951; BAC49670.1; -.
 KW Complete proteome.
 SQ SEQUENCE 91 AA; 10366 MW; BD512A98AC3F55AC CRC64;

Query Match 75.0%; Score 6; DB 16; Length 91;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 NLDAEF 8
 |||||
 Db 28 NLDAEF 33

RESULT 3

Q80PA8

ID Q80PA8 PRELIMINARY; PRT; 101 AA.

AC Q80PA8;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Orf6 (Fragment).
 OS Spodoptera litura nucleopolyhedrovirus.
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
 OC Nucleopolyhedrovirus.
 OX NCBI_TaxID=46242;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Jain M., Das R.H.;
 RT "Molecular characterization of the structural glycoprotein gp41 gene
 RT of Spodoptera litura nucleopolyhedrosis virus.";
 RL Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Jain M., Das R.H.;
 RT "Nucleotide sequence of a 4053bp fragment of the SpltNPV genome and
 RT comparison with the AcNPV genome.";
 RL Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF445192; AAO43572.1; -.
 FT NON_TER 101 101
 SQ SEQUENCE 101 AA; 12174 MW; 0D9DE836AA4CAFE5 CRC64;

Query Match 75.0%; Score 6; DB 12; Length 101;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NLDAEF 8
 |||||
 Db 96 NLDAEF 101

RESULT 4

Q87ZB6

ID Q87ZB6 PRELIMINARY; PRT; 173 AA.
 AC Q87ZB6;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Conserved hypothetical protein.
 GN PSPTO3513.
 OS Pseudomonas syringae (pv. tomato).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=323;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DC3000;
 RA Buell R., Joardar V., Khouri H., Fedorova N., Tran B., Russell D.,
 RA Berry K., Utterback T., Van Aken S., Feldblyum T., Gwinn M.,
 RA Dodson R., DeBoy R., Durkin A., Kolonay J., Madupu R., Daugherty S.,
 RA Brinkac L., Beanan M., Haft D., Selengut J., Nelson W., Davidsen T.,
 RA White O., Fraser C., Collmer A.;
 RT "Complete sequence of Pseudomonas syringae.";
 RL Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AE016868; AAO56988.1; -.
DR TIGR; PSPTO3513; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 173 AA; 19395 MW; 6FB8ACC113B365C2 CRC64;

Query Match 75.0%; Score 6; DB 16; Length 173;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VNLDAA 7
| | | | |
Db 137 VNLDAA 142

RESULT 5

Q82WI7

ID Q82WI7 PRELIMINARY; PRT; 221 AA.
AC Q82WI7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE LeuD; 3-isopropylmalate dehydratase small subunit (EC 4.2.1.33).
GN LEUD OR NE0687.
OS Nitrosomonas europaea.
OC Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
OC Nitrosomonadaceae; Nitrosomonas.
OX NCBI_TaxID=915;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19718 / IFO 14298;
RX MEDLINE=22586410; PubMed=12700255;
RA Chain P., Lamerdin J.E., Larimer F.W., Regala W., Lao V., Land M.,
RA Hauser L., Hooper A.B., Klotz M.G., Norton J., Sayavedra-Soto L.A.,
RA Arciero D.M., Hommes N.G., Whittaker M.M., Arp D.J.;
RT "Complete genome sequence of the ammonia-oxidizing bacterium and
RT obligate chemolithoautotroph Nitrosomonas europaea."
RL J. Bacteriol. 185:2759-2773(2003).
DR EMBL; BX321858; CAD84598.1; -.
DR GO; GO:0009316; C:3-isopropylmalate dehydratase complex; IEA.
DR GO; GO:0003861; F:3-isopropylmalate dehydratase activity; IEA.
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0009098; P:leucine biosynthesis; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR000573; Aconitase_C.
DR InterPro; IPR004431; LeuD.
DR Pfam; PF00694; Aconitase_C; 1.
DR TIGRFAMs; TIGR00171; leuD; 1.
KW Lyase; Complete proteome.
SQ SEQUENCE 221 AA; 25456 MW; 63E2A21073AE8C88 CRC64;

Query Match 75.0%; Score 6; DB 16; Length 221;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDA 6
| | | | |
Db 151 EVNLDA 156

RESULT 6

Q8A4M0

ID Q8A4M0 PRELIMINARY; PRT; 281 AA.
 AC Q8A4M0;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Conserved hypothetical protein.
 GN BT2579.
 OS Bacteroides thetaiotaomicron.
 OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
 OC Bacteroidaceae; Bacteroides.
 OX NCBI_TaxID=818;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VPI-5482 / ATCC 29148;
 RX MEDLINE=22550858; PubMed=12663928;
 RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
 RA Chiang H.C., Hooper L.V., Gordon J.I.;
 RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
 RL Science 299:2074-2076(2003).
 DR EMBL; AE016936; AAO77686.1; -.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0016233; P:telomere capping; IEA.
 DR InterPro; IPR003415; Telo_bind_alpha.
 DR ProDom; PD018295; Telo_bind_alpha; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 281 AA; 33830 MW; 400ADEE36AC9563F CRC64;

Query Match 75.0%; Score 6; DB 16; Length 281;
 Best Local Similarity 100.0%; Pred. No. 63;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VNLD AE 7
 |||||
 Db 264 VNLD AE 269

RESULT 7

Q93ET9

ID Q93ET9 PRELIMINARY; PRT; 299 AA.
 AC Q93ET9;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Aminoglycoside phosphotransferase.
 GN APH(2')-IB.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21441138; PubMed=11557456;

RA Chow J.W., Kak V., You I., Kao S.J., Petrin J., Clewell D.B.,
 RA Lerner S.A., Miller G.H., Shaw K.J.;
 RT "Aminoglycoside Resistance Genes aph(2')-Ib and aac(6')-Im Detected
 RT Together in Strains of both Escherichia coli and Enterococcus
 RT faecium.";
 RL Antimicrob. Agents Chemother. 45:2691-2694(2001).
 DR EMBL; AF337947; AAK63040.1; -.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR002575; APH.
 DR InterPro; IPR008266; Tyr_pkinase_AS.
 DR Pfam; PF01636; APH; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 KW Transferase.
 SQ SEQUENCE 299 AA; 35350 MW; 6A69D4F6E6901C81 CRC64;

Query Match 75.0%; Score 6; DB 2; Length 299;
 Best Local Similarity 100.0%; Pred. No. 66;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VNLD AE 7
 |||||
 Db 2 VNLD AE 7

RESULT 8

Q9EVD7

ID Q9EVD7 PRELIMINARY; PRT; 299 AA.
 AC Q9EVD7;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Aminoglycoside phosphotransferase.
 GN APH(2')-IB.
 OS Enterococcus faecium (Streptococcus faecium).
 OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
 OX NCBI_TaxID=1352;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SF11770;
 RX MEDLINE=20448770; PubMed=10991878;
 RA Kao S.J., You I., Clewell D.B., Donabedian S.M., Zervos M.J.,
 RA Petrin J., Shaw K.J., Chow J.W.;
 RT "Detection of the high-level aminoglycoside resistance gene aph(2')-Ib
 RT in Enterococcus faecium.";
 RL Antimicrob. Agents Chemother. 44:2876-2879(2000).
 DR EMBL; AF207840; AAG13458.1; -.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR002575; APH.
 DR InterPro; IPR008266; Tyr_pkinase_AS.
 DR Pfam; PF01636; APH; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

KW Transferase.
SQ SEQUENCE 299 AA; 35353 MW; 8B99DB5020FDAE23 CRC64;

Query Match 75.0%; Score 6; DB 2; Length 299;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VNLD AE 7
 |||||
Db 2 VNLD AE 7

RESULT 9

Q933C0
ID Q933C0 PRELIMINARY; PRT; 304 AA.
AC Q933C0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE NodI protein.
GN NODI.
OS Rhizobium tropici.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
OX NCBI_TaxID=398;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CIAT899;
RX MEDLINE=97002746; PubMed=8850086;
RA Folch-Mallol J.L., Marroqui S., Sousa C., Manyani H., Lopez-Lara I.,
RA van der Drift K.M.G.M., Haverkamp J., Quinto C., Gil-Serrano A.,
RA Thomas-Oates J., Spaink H.P., Megias M.;
RT "Characterization of Rhizobium tropici CIAT899 nodulation factors: The
RT role of nodH and nodPQ genes in their sulfation.";
RL Mol. Plant Microbe Interact. 9:151-163(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CIAT899;
RA Manyani H., Sousa C., Soria-Diaz M.E., Gil-Serrano A., Megias M.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=CIAT899;
RX MEDLINE=21360362; PubMed=11467733;
RA Manyani H., Sousa C., Soria Diaz M.E., Gil-Serrano A., Megias M.;
RT "Regulation of nod factor sulphation genes in Rhizobium tropici
RT CIAT899.";
RL Can. J. Microbiol. 47:574-579(2001).
CC -!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
DR EMBL; X87608; CAC39128.1; -.
DR EMBL; AY029295; AAL02416.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti. . .; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0009877; P:nodulation; IEA.

DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR003593; AAA_ATPase.
 DR InterPro; IPR003439; ABC_transporter.
 DR InterPro; IPR005978; ABC_transptNodI.
 DR Pfam; PF00005; ABC_tran; 1.
 DR ProDom; PD000006; ABC_transporter; 1.
 DR SMART; SM00382; AAA; 1.
 DR TIGRFAMs; TIGR01288; nodI; 1.
 DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
 DR PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
 KW ATP-binding; Transport.
 SQ SEQUENCE 304 AA; 33635 MW; A9A3A462DCEE5E92 CRC64;

Query Match 75.0%; Score 6; DB 2; Length 304;
 Best Local Similarity 100.0%; Pred. No. 67;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NLDAEF 8
 |||||
 Db 88 NLDAEF 93

RESULT 10

Q8HOB0

ID Q8HOB0 PRELIMINARY; PRT; 308 AA.
 AC Q8HOB0;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Putative gibberellin 20-oxidase.
 GN OSJNBA0096G08.6.
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nipponbare;
 RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Kim M.M.,
 RA Overton II L.L., Bera J.J., Tsitrin T., Krol M.I., Jarrahi B.B.,
 RA Jin S.S., Koo H., Zismann V., Hsiao J., Blunt S., Vanaken S.S.,
 RA Utterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J., Suh B.B.,
 RA Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
 RT "Oryza sativa chromosome 10 BAC OSJNBa0096G08 genomic sequence."
 RL Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AC078894; AAO00709.1; -.
 DR GO; GO:0005506; F:iron ion binding; IEA.
 DR GO; GO:0016216; F:isopenicillin-N synthase activity; IEA.
 DR GO; GO:0017000; P:antibiotic biosynthesis; IEA.
 DR InterPro; IPR005123; 2OG-FeII_Oxy.
 DR InterPro; IPR002283; IPN_synth.
 DR Pfam; PF03171; 2OG-FeII_Oxy; 1.
 DR PRINTS; PR00682; IPNSYNTHASE.
 SQ SEQUENCE 308 AA; 34541 MW; AC6F16A95D78D905 CRC64;

Query Match 75.0%; Score 6; DB 10; Length 308;

Best Local Similarity 100.0%; Pred. No. 68;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 NLDAEF 8
|||||
Db 155 NLDAEF 160

RESULT 11

Q7V5K6

ID Q7V5K6 PRELIMINARY; PRT; 319 AA.
AC Q7V5K6;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE DnaJ3 protein.
GN DNAJ3 OR PMT1548.
OS Prochlorococcus marinus (strain MIT 9313).
OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID=74547;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22825698; PubMed=12917642;
RA Rocap G., Larimer F.W., Lamerdin J., Malfatti S., Chain P.,
RA Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,
RA Johnson Z.I., Land M., Lindell D., Post A.F., Regala W., Shah M.,
RA Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
RA Webb E.A., Zinser E.R., Chisholm S.W.;
RT "Genome divergence in two Prochlorococcus ecotypes reflects oceanic
RT niche differentiation.";
RL Nature 424:1042-1047(2003).
DR EMBL; BX572099; CAE21723.1; -.
KW Complete proteome.
SQ SEQUENCE 319 AA; 34597 MW; 8026B72577603912 CRC64;

Query Match 75.0%; Score 6; DB 16; Length 319;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VNLD AE 7
|||||
Db 141 VNLD AE 146

RESULT 12

Q88P95

ID Q88P95 PRELIMINARY; PRT; 324 AA.
AC Q88P95;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE KpsF/GutQ family protein.
GN PP0957.
OS Pseudomonas putida (strain KT2440).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.

OX NCBI_TaxID=160488;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22423060; PubMed=12534463;
 RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
 RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
 RA Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J.,
 RA Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I.,
 RA Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazzez A.,
 RA Utterback T., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H.,
 RA Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,
 RA Kiewitz C., Eisen J., Timmis K.N., Duesterhoeft A., Tümmeler B.,
 RA Fraser C.M.;
 RT "Complete genome sequence and comparative analysis of the
 RT metabolically versatile *Pseudomonas putida* KT2440.";
 RL Environ. Microbiol. 4:799-808(2002).
 DR EMBL; AE016777; AAN66582.1; -.
 DR TIGR; PP0957; -.
 DR GO; GO:0005529; F:sugar binding; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR000644; CBS_domain.
 DR InterPro; IPR001347; SIS.
 DR Pfam; PF00571; CBS; 2.
 DR Pfam; PF01380; SIS; 1.
 KW Complete proteome.
 SQ SEQUENCE 324 AA; 34397 MW; 67CEF2C1606E962F CRC64;

Query Match 75.0%; Score 6; DB 16; Length 324;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVNLDA 6
 |||||
 Db 137 EVNLDA 142

RESULT 13

Q7U4X9

ID Q7U4X9 PRELIMINARY; PRT; 324 AA.
 AC Q7U4X9;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE DnaJ3 protein.
 GN DNAJ3 OR SYNW1934.
 OS *Synechococcus* sp. (strain WH8102).
 OC Bacteria; Cyanobacteria; Chroococcales; *Synechococcus*.
 OX NCBI_TaxID=84588;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22825697; PubMed=12917641;
 RA Palenik B., Brahamsha B., Larimer F.W., Land M., Hauser L., Chain P.,
 RA Lamerdin J., Regala W., Allen E.E., McCarren J., Paulsen I.,
 RA Dufresne A., Partensky F., Webb E.A., Waterbury J.;
 RT "The genome of a motile marine *Synechococcus*.";
 RL Nature 424:1037-1042(2003).
 DR EMBL; BX569694; CAE08449.1; -.

KW Complete proteome.

SQ SEQUENCE 324 AA; 34972 MW; 8BD4931073F87B31 CRC64;

Query Match 75.0%; Score 6; DB 16; Length 324;

Best Local Similarity 100.0%; Pred. No. 71;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VNLD AE 7

|||||

Db 146 VNLD AE 151

RESULT 14

Q9HVVW0

ID Q9HVVW0 PRELIMINARY; PRT; 326 AA.

AC Q9HVVW0;

DT 01-MAR-2001 (TrEMBLrel. 16, Created)

DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Hypothetical protein PA4457.

GN PA4457.

OS Pseudomonas aeruginosa.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

OC Pseudomonadaceae; Pseudomonas.

OX NCBI_TaxID=287;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 15692 / PA01;

RX MEDLINE=20437337; PubMed=10984043;

RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,

RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,

RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,

RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;

RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an

RT opportunistic pathogen.";

RL Nature 406:959-964(2000).

DR EMBL; AE004860; AAG07845.1; -.

DR PIR; A83087; A83087.

DR GO; GO:0005529; F:sugar binding; IEA.

DR GO; GO:0005975; P:carbohydrate metabolism; IEA.

DR InterPro; IPR000644; CBS_domain.

DR InterPro; IPR004800; KpsF.

DR InterPro; IPR001347; SIS.

DR Pfam; PF00571; CBS; 2.

DR Pfam; PF01380; SIS; 1.

DR SMART; SM00116; CBS; 2.

DR TIGRFAMs; TIGR00393; kpsF; 1.

KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 326 AA; 34197 MW; 510B3190C0F92C51 CRC64;

Query Match 75.0%; Score 6; DB 16; Length 326;

Best Local Similarity 100.0%; Pred. No. 71;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDA 6

|||||
Db 139 EVNLDA 144

RESULT 15

Q9AHQ9

ID Q9AHQ9 PRELIMINARY; PRT; 352 AA.
AC Q9AHQ9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE N10-formyltetrahydrofolate synthetase (EC 6.3.4.3) (Fragment).
OS Gamma-proteobacterium Hot 75m4.
OC Bacteria; environmental samples.
OX NCBI_TaxID=77133;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21141862; PubMed=11229939;
RA Leaphart A.B., Lovell C.R.;
RT "Recovery and Analysis of Formyltetrahydrofolate Synthetase Gene
RT Sequences from Natural Populations of Acetogenic Bacteria.";
RL Appl. Environ. Microbiol. 67:1392-1395(2001).
DR EMBL; AF295714; AAK20259.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004329; F:formate-tetrahydrofolate ligase activity; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0009396; P:folic acid and derivative biosynthesis; IEA.
DR InterPro; IPR000559; Fmtethyd_synth.
DR Pfam; PF01268; FTHFS; 1.
DR PROSITE; PS00722; FTHFS_2; 1.
KW Ligase.
FT NON_TER 1 1
FT NON_TER 352 352
SQ SEQUENCE 352 AA; 37942 MW; FC473D2236908EC9 CRC64;

Query Match 75.0%; Score 6; DB 2; Length 352;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVNLDA 6
|||||
Db 215 EVNLDA 220

RESULT 16

Q8H0A8

ID Q8H0A8 PRELIMINARY; PRT; 357 AA.
AC Q8H0A8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative gibberellin 20-oxidase.
GN OSJNBA0096G08.8.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.

OX NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nipponbare;
 RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Kim M.M.,
 RA Overton II L.L., Bera J.J., Tsitrin T., Krol M.I., Jarrahi B.B.,
 RA Jin S.S., Koo H., Zismann V., Hsiao J., Blunt S., Vanaken S.S.,
 RA Utterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J., Suh B.B.,
 RA Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
 RT "Oryza sativa chromosome 10 BAC OSJNBa0096G08 genomic sequence.";
 RL Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nipponbare;
 RA The Rice Chromosome 10 Sequencing Consortium;
 RT "In-depth view of structure, activity, and evolution of rice
 RT chromosome 10.";
 RL Science 300:1566-1569(2003).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nipponbare;
 RA Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;
 RL Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AC078894; AAO00707.1; -.
 DR EMBL; AE017113; AAP54689.1; -.
 DR GO; GO:0005506; F:iron ion binding; IEA.
 DR GO; GO:0016216; F:isopenicillin-N synthase activity; IEA.
 DR GO; GO:0017000; P:antibiotic biosynthesis; IEA.
 DR InterPro; IPR005123; 2OG-FeII_Oxy.
 DR InterPro; IPR002283; IPN_synth.
 DR Pfam; PF03171; 2OG-FeII_Oxy; 1.
 DR PRINTS; PR00682; IPNSYNTHASE.
 SQ SEQUENCE 357 AA; 39386 MW; 319BE07F54FA6DC0 CRC64;

Query Match 75.0%; Score 6; DB 10; Length 357;
 Best Local Similarity 100.0%; Pred. No. 77;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NLD AEF 8
 |||||
 Db 198 NLD AEF 203

RESULT 17

Q8LNJ6

ID Q8LNJ6 PRELIMINARY; PRT; 381 AA.
 AC Q8LNJ6;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Putative gibberellin oxidase.
 GN OSJNB0028C01.33.
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 OX NCBI_TaxID=39947;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nipponbare;
 RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Kim M.M.,
 RA Overton II L.L., Bera J.J., Tsitrin T., Krol M.I., Jarrahi B.B.,
 RA Jin S.S., Koo H., Zismann V., Hsiao J., Blunt S., Vanaken S.S.,
 RA Utterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J., Suh B.B.,
 RA Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
 RT "Oryza sativa chromosome 10 BAC OSJNBb0028C01 genomic sequence.";
 RL Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.

RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nipponbare;
 RA The Rice Chromosome 10 Sequencing Consortium;
 RT "In-depth view of structure, activity, and evolution of rice
 RT chromosome 10.";
 RL Science 300:1566-1569(2003).

RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nipponbare;
 RA Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;
 RL Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AC079029; AAM92286.1; -.
 DR EMBL; AE017113; AAP54688.1; -.
 DR Gramene; Q8LNJ6; -.
 DR GO; GO:0005506; F:iron ion binding; IEA.
 DR GO; GO:0016216; F:isopenicillin-N synthase activity; IEA.
 DR GO; GO:0017000; P:antibiotic biosynthesis; IEA.
 DR InterPro; IPR005123; 2OG-FeII_Oxy.
 DR InterPro; IPR002283; IPN_synth.
 DR Pfam; PF03171; 2OG-FeII_Oxy; 1.
 DR PRINTS; PR00682; IPNSYNTHASE.
 SQ SEQUENCE 381 AA; 42401 MW; 7F21802141337B55 CRC64;

Query Match 75.0%; Score 6; DB 10; Length 381;
 Best Local Similarity 100.0%; Pred. No. 82;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 NLD AEF 8
 |||||
 Db 228 NLD AEF 233

RESULT 18

Q8AVI2
 ID Q8AVI2 PRELIMINARY; PRT; 436 AA.
 AC Q8AVI2;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Similar to keratin 18 (Fragment).
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]

RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA Klein S., Strausberg R.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC042269; AAH42269.1; -.
 DR GO; GO:0005882; C:intermediate filament; IEA.
 DR InterPro; IPR001664; IF.
 DR InterPro; IPR002957; Keratin_I.
 DR Pfam; PF00038; filament; 1.
 DR PRINTS; PR01248; TYPE1KERATIN.
 DR PROSITE; PS00226; IF; 1.
 KW Keratin.
 FT NON_TER 1 1
 SQ SEQUENCE 436 AA; 48322 MW; F3466A556C5B729D CRC64;

Query Match 75.0%; Score 6; DB 13; Length 436;
 Best Local Similarity 100.0%; Pred. No. 92;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VNLDAE 7
 |||||
 Db 288 VNLDAE 293

RESULT 19

Q87UP7

ID Q87UP7 PRELIMINARY; PRT; 500 AA.
 AC Q87UP7;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Exopolyphosphatase.
 GN PPX OR PSPTO5249.
 OS Pseudomonas syringae (pv. tomato).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=323;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DC3000;
 RA Buell R., Joardar V., Khouri H., Fedorova N., Tran B., Russell D.,
 RA Berry K., Utterback T., Van Aken S., Feldblyum T., Gwinn M.,
 RA Dodson R., DeBoy R., Durkin A., Kolonay J., Madupu R., Daugherty S.,
 RA Brinkac L., Beanan M., Haft D., Selengut J., Nelson W., Davidsen T.,
 RA White O., Fraser C., Collmer A.;
 RT "Complete sequence of Pseudomonas syringae."
 RL Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AE016875; AAO58675.1; -.
 DR TIGR; PSPTO5249; -.
 DR GO; GO:0008784; F:alanine racemase activity; IEA.
 DR GO; GO:0006522; P:alanine metabolism; IEA.
 DR InterPro; IPR000821; Ala_racemase.
 DR InterPro; IPR003695; Ppx_GppA.
 DR Pfam; PF02541; Ppx-GppA; 1.
 DR PROSITE; PS00395; ALANINE_RACEMASE; 1.
 KW Complete proteome.
 SQ SEQUENCE 500 AA; 56248 MW; 1F3123C8483632DB CRC64;

Query Match 75.0%; Score 6; DB 16; Length 500;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 NLDAEF 8
| | | | |
Db 463 NLDAEF 468

RESULT 20

Q97XQ7

ID Q97XQ7 PRELIMINARY; PRT; 802 AA.
AC Q97XQ7;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein SSO1653.
GN SSO1653.
OS Sulfolobus solfataricus.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=2287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 35092 / DSM 1617 / P2;
RX MEDLINE=21332296; PubMed=11427726;
RA She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
RA Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
RA De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,
RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
RA Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;
RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
DR EMBL; AE006779; AAK41866.1; -.
DR PIR; C90326; C90326.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0008026; F:ATP dependent helicase activity; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR000330; SNF2_N.
DR Pfam; PF00176; SNF2_N; 1.
DR SMART; SM00487; DEXDc; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 802 AA; 92852 MW; 80F86655C9F5040A CRC64;

Query Match 75.0%; Score 6; DB 17; Length 802;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDA 6
| | | | |
Db 292 EVNLDA 297

RESULT 21

Q9VI82

ID Q9VI82 PRELIMINARY; PRT; 822 AA.
AC Q9VI82;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CG1234 protein (LD35257P).
GN CG1234.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
 RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanenvong S., Wan K.,
 RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AE003672; AAF54043.1; -.
 DR EMBL; AY051854; AAK93278.1; -.
 DR FlyBase; FBgn0037489; CG1234.
 DR GO; GO:0004197; F:cysteine-type endopeptidase activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR008938; ARM.
 DR InterPro; IPR005612; CBF.
 DR InterPro; IPR000169; SHprot_acsite.
 DR Pfam; PF03914; CBF; 1.
 DR PROSITE; PS00639; TH1OL_PROTEASE_HIS; 1.
 SQ SEQUENCE 822 AA; 94492 MW; B6B724F9F83A4BC8 CRC64;

Query Match 75.0%; Score 6; DB 5; Length 822;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VNLDAAE 7
 |||||
 Db 449 VNLDAAE 454

RESULT 22

Q961M8

ID Q961M8 PRELIMINARY; PRT; 839 AA.

AC Q961M8;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE GH15453p.

GN DHC64C OR CG7507.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Berkeley;

RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,

RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,

RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,

RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanenvong S., Wan K.,

RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;

RL Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AY051501; AAK92925.1; -.

DR FlyBase; FBgn0010349; Dhc64C.

DR GO; GO:0045169; C:fusome; NAS.

DR GO; GO:0008567; F:dynein ATPase activity; IDA.

DR GO; GO:0003777; F:microtubule motor activity; IDA.

DR GO; GO:0007098; P:centrosome cycle; IMP.
 DR GO; GO:0007292; P:female gamete generation; IMP.
 DR GO; GO:0045478; P:fusome organization and biogenesis; NAS.
 DR GO; GO:0007018; P:microtubule-based movement; IDA.
 DR GO; GO:0007294; P:oocyte cell fate determination (sensu Insecta); IMP.
 DR InterPro; IPR004273; Dynein_heavy.
 DR Pfam; PF03028; Dynein_heavy; 1.
 SQ SEQUENCE 839 AA; 94472 MW; 038B81350D706C0C CRC64;

Query Match 75.0%; Score 6; DB 5; Length 839;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 NLDAEF 8
 |||||
 Db 85 NLDAEF 90

RESULT 23

Q9KRY9

ID Q9KRY9 PRELIMINARY; PRT; 868 AA.
 AC Q9KRY9;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Aminopeptidase N.
 GN VC1494.
 OS Vibrio cholerae.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrio.
 OX NCBI_TaxID=666;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=El Tor N16961 / Serotype O1;
 RX MEDLINE=20406833; PubMed=10952301;
 RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
 RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
 RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
 RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
 RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
 RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
 RA Fraser C.M.;
 RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
 RT cholerae.";
 RL Nature 406:477-483(2000).
 DR EMBL; AE004227; AAF94649.1; -.
 DR PIR; G82193; G82193.
 DR MEROPS; M01.005; -.
 DR TIGR; VC1494; -.
 DR GO; GO:0004179; F:membrane alanyl aminopeptidase activity; IEA.
 DR GO; GO:0008237; F:metallopeptidase activity; IEA.
 DR GO; GO:0008270; F:zinc ion binding; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR001930; Peptidase_M1.
 DR InterPro; IPR006025; Pept_M_Zn_BS.
 DR Pfam; PF01433; Peptidase_M1; 1.
 DR PRINTS; PR00756; ALADIPTASE.

DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Complete proteome.
SQ SEQUENCE 868 AA; 98404 MW; 81A56B4B7A00A82F CRC64;

Query Match 75.0%; Score 6; DB 16; Length 868;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 NLDAEF 8
| | | | |
Db 606 NLDAEF 611

RESULT 24

Q7WMP8

ID Q7WMP8 PRELIMINARY; PRT; 894 AA.
AC Q7WMP8;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Aconitate hydratase (EC 4.2.1.3).
GN ACN OR ACNA OR BB1342.
OS Bordetella bronchiseptica (Alcaligenes bronchisepticus).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=518;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RB50 / ATCC BAA-588;
RX MEDLINE=22827954; PubMed=12910271;
RA Parkhill J., Sebahia M., Preston A., Murphy L.D., Thomson N.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdeno-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,
RA Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica."
RL Nat. Genet. 35:32-40(2003).
DR EMBL; BX640441; CAE31840.1; -.
KW Lyase; Complete proteome.
SQ SEQUENCE 894 AA; 96617 MW; 560A1DE58317C882 CRC64;

Query Match 75.0%; Score 6; DB 16; Length 894;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 NLDAEF 8
| | | | |
Db 147 NLDAEF 152

RESULT 25

Q7WB80

ID Q7WB80 PRELIMINARY; PRT; 894 AA.
AC Q7WB80;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Aconitase hydratase (EC 4.2.1.3).
GN ACN OR ACNA OR BPP1126.
OS Bordetella parapertussis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=519;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=12822 / ATCC BAA-587;
RX MEDLINE=22827954; PubMed=12910271;
RA Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdano-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,
RA Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica."
RL Nat. Genet. 35:32-40(2003).
DR EMBL; BX640426; CAE36427.1; -.
KW Lyase; Complete proteome.
SQ SEQUENCE 894 AA; 96559 MW; D131C525010B3C75 CRC64;

Query Match 75.0%; Score 6; DB 16; Length 894;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 NLDAEF 8
| | | | |
Db 147 NLDAEF 152

RESULT 26

Q8DL57

ID Q8DL57 PRELIMINARY; PRT; 1324 AA.
AC Q8DL57;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RNA polymerase beta prime subunit.
GN RPOC2 OR TLL0640.
OS Synechococcus elongatus (Thermosynechococcus elongatus).
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX NCBI_TaxID=32046;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BP-1;

RX MEDLINE=22225144; PubMed=12240834;
 RA Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S.,
 RA Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y.,
 RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N.,
 RA Shimpō S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
 RT "Complete genome structure of the thermophilic cyanobacterium
 RT Thermosynechococcus elongatus BP-1.";
 RL DNA Res. 9:123-130(2002).
 DR EMBL; AP005371; BAC08191.1; -.
 DR GO; GO:0003899; F:DNA-directed RNA polymerase activity; IEA.
 DR GO; GO:0006350; P:transcription; IEA.
 DR InterPro; IPR007066; RNA_pol_Rpb1_3.
 DR InterPro; IPR007083; RNA_pol_Rpb1_4.
 DR InterPro; IPR007081; RNA_pol_Rpb1_5.
 DR Pfam; PF04983; RNA_pol_Rpb1_3; 1.
 DR Pfam; PF05000; RNA_pol_Rpb1_4; 1.
 DR Pfam; PF04998; RNA_pol_Rpb1_5; 1.
 KW Complete proteome.
 SQ SEQUENCE 1324 AA; 144701 MW; 2A82FE2C94B54976 CRC64;

Query Match 75.0%; Score 6; DB 16; Length 1324;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VNLD AE 7
 |||||
 Db 454 VNLD AE 459

RESULT 27

Q8INT5

ID Q8INT5 PRELIMINARY; PRT; 1469 AA.
 AC Q8INT5;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE CG31623-PA.
 GN DTR OR CG31623.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
 RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarri C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
 RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
 RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
 RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
 RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
 RA Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A.,
 RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
 RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
 RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
 RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
 RA Phouanenvong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
 RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
 RT "Sequencing of *Drosophila melanogaster* genome.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 RA Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,
 RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
 RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
 RA Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
 RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
 RT "Annotation of *Drosophila melanogaster* genome.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.

RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA FlyBase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AE003670; AAN11119.1; -.
 DR FlyBase; FBgn0023090; dtr.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR007092; LRR_SDS22.
 DR Pfam; PF00560; LRR; 4.
 SQ SEQUENCE 1469 AA; 166591 MW; D42181269A4651E1 CRC64;

Query Match 75.0%; Score 6; DB 5; Length 1469;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 NLDAEF 8
 |||||
 Db 1016 NLDAEF 1021

RESULT 28

Q9VZ83

ID Q9VZ83 PRELIMINARY; PRT; 4639 AA.
 AC Q9VZ83;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE CG7507 protein.
 GN DHC64C OR CG7507.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarri C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
 RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
 RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
 RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
 RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
 RA Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A.,
 RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
 RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
 RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
 RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
 RA Phouanenvong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
 RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
 RT "Sequencing of *Drosophila melanogaster* genome.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 RA Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,
 RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
 RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
 RA Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
 RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
 RT "Annotation of *Drosophila melanogaster* genome.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA FlyBase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AE003482; AAF47942.3; -.
 DR FlyBase; FBgn0010349; Dhc64C.
 DR GO; GO:0045169; C:fusome; NAS.
 DR GO; GO:0008567; F:dynein ATPase activity; IDA.
 DR GO; GO:0003777; F:microtubule motor activity; IDA.
 DR GO; GO:0007098; P:centrosome cycle; IMP.
 DR GO; GO:0007292; P:female gamete generation; IMP.
 DR GO; GO:0045478; P:fusome organization and biogenesis; NAS.
 DR GO; GO:0007018; P:microtubule-based movement; IDA.
 DR GO; GO:0007294; P:oocyte cell fate determination (sensu Insecta); IMP.
 DR InterPro; IPR003593; AAA_ATPase.
 DR InterPro; IPR001064; Crystallin.
 DR InterPro; IPR004273; Dynein_heavy.
 DR InterPro; IPR000169; SHprot_acsite.
 DR Pfam; PF03028; Dynein_heavy; 1.
 DR SMART; SM00382; AAA; 4.
 DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
 DR PROSITE; PS00639; THIOL_PROTEASE_HIS; 1.
 KW ATP-binding.
 SQ SEQUENCE 4639 AA; 530172 MW; 2A3D4F1F8BE52096 CRC64;

Query Match 75.0%; Score 6; DB 5; Length 4639;
 Best Local Similarity 100.0%; Pred. No. 7.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NLDAEF 8
 |||||
 Db 3885 NLDAEF 3890

RESULT 29

Q8CG65

ID Q8CG65 PRELIMINARY; PRT; 4998 AA.
 AC Q8CG65;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE SCO-spondin.
 GN SCO-SPONDIN.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ICR; TISSUE=Brain;
 RA Goncalves N., Simon-Chazottes D., Creveaux I., Meinier A.,
 RA Guenet J-L., Meinier R.;
 RT "Characterization, spatio-temporal expression and chromosomal
 RT assignment of mouse SCO-spondin."
 RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AJ491857; CAD42654.1; -.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005507; F:copper ion binding; IEA.
 DR GO; GO:0005489; F:electron transporter activity; IEA.
 DR GO; GO:0005179; F:hormone activity; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.

DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR000923; BlueCu_1.
 DR InterPro; IPR006207; Cys_knot_C.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR000421; FA58_C.
 DR InterPro; IPR001545; Gly_hormoneB.
 DR InterPro; IPR002172; LDL_receptor_A.
 DR InterPro; IPR002919; TIL_Cysrich.
 DR InterPro; IPR000884; TSP1.
 DR InterPro; IPR008085; TSP_1.
 DR InterPro; IPR006552; VC_out.
 DR InterPro; IPR001007; VWF_C.
 DR InterPro; IPR001846; VWF_D.
 DR Pfam; PF00754; F5_F8_type_C; 1.
 DR Pfam; PF00057; ldl_recept_a; 10.
 DR Pfam; PF01826; TIL; 10.
 DR Pfam; PF00090; tsp_1; 25.
 DR Pfam; PF00093; vwc; 1.
 DR Pfam; PF00094; vwd; 3.
 DR PRINTS; PR00261; LDLRECEPTOR.
 DR PRINTS; PR01705; TSP1REPEAT.
 DR SMART; SM00192; LDLa; 10.
 DR SMART; SM00209; TSP1; 25.
 DR SMART; SM00214; VWC; 4.
 DR SMART; SM00215; VWC_out; 9.
 DR SMART; SM00216; VWD; 2.
 DR PROSITE; PS00196; COPPER_BLUE; 1.
 DR PROSITE; PS01225; CTCK_2; 1.
 DR PROSITE; PS01186; EGF_2; 2.
 DR PROSITE; PS50022; FA58C_3; 1.
 DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 2.
 DR PROSITE; PS01209; LDLRA_1; 8.
 DR PROSITE; PS50068; LDLRA_2; 10.
 DR PROSITE; PS50092; TSP1; 25.
 DR PROSITE; PS01208; VWFC_1; 1.
 DR PROSITE; PS50184; VWFC_2; 2.
 SQ SEQUENCE 4998 AA; 535019 MW; DA2ABA8DA47DF225 CRC64;

Query Match 75.0%; Score 6; DB 11; Length 4998;
 Best Local Similarity 100.0%; Pred. No. 7.7e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 NLDAEF 8
 |||||
 Db 2863 NLDAEF 2868

RESULT 30

Q88UM4

ID Q88UM4 PRELIMINARY; PRT; 46 AA.
 AC Q88UM4;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Prophage Lp2 protein 11.
 GN LP_2446.
 OS Lactobacillus plantarum.

OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 OC Lactobacillus.
 OX NCBI_TaxID=1590;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NCIMB 8826 / WCFS1;
 RX MEDLINE=22480296; PubMed=12566566;
 RA Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,
 RA Kuipers O.P., Leer R., Tarchini R., Peters S.A., Sandbrink H.M.,
 RA Fiers M.W.E.J., Stiekema W., Klein Lankhorst R.M., Bron P.A.,
 RA Hoffer S.M., Nierop Groot M.N., Kerkhoven R., De Vries M., Ursing B.,
 RA De Vos W.M., Siezen R.J.;
 RT "Complete genome sequence of Lactobacillus plantarum WCFS1."
 RL Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995(2003).
 DR EMBL; AL935259; CAD64752.1; -.
 KW Complete proteome.
 SQ SEQUENCE 46 AA; 5193 MW; 9E00259EEEA59996 CRC64;

Query Match 62.5%; Score 5; DB 16; Length 46;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LDAEF 8
 |||||
 Db 33 LDAEF 37

RESULT 31

Q9PVI4

ID Q9PVI4 PRELIMINARY; PRT; 49 AA.
 AC Q9PVI4;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Regulator of G-protein signalling 4 (Fragment).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Dorsal root ganglion;
 RA Schiff M., Jordan J.D., Ortiz D.F., De Vries L., Fischer T.,
 RA Farquhar M.G., Diverse-Pierluissi M.;
 RT "Selective effects of GAIP and RGS4 on desensitization of neuronal
 RT signalling pathways."
 RL Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF090091; AAF00033.1; -.
 DR HSSP; P49799; 1AGR.
 DR GO; GO:0004871; F:signal transducer activity; IEA.
 DR InterPro; IPR000342; Regl_Gprotein.
 DR Pfam; PF00615; RGS; 1.
 DR PROSITE; PS50132; RGS; 1.
 FT NON_TER 1 1
 FT NON_TER 49 49
 SQ SEQUENCE 49 AA; 5701 MW; 0E6F5802FAF55973 CRC64;

Query Match 62.5%; Score 5; DB 13; Length 49;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLD 5
|||||
Db 10 EVNLD 14

RESULT 32

Q8KM85

ID Q8KM85 PRELIMINARY; PRT; 50 AA.
AC Q8KM85;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
OS Mycoplasma suis.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=57372;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=54/96;
RA Hoelzle L.E., Adelt D., Hoelzle K., Heinritzi K., Wittenbrink M.M.;
RT "Purification and analysis of Mycoplasma suis (Eperythrozoon suis) DNA
RT from porcine blood."
RL Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AJ504999; CAD44546.1; -.
KW Hypothetical protein.
SQ SEQUENCE 50 AA; 5767 MW; 93B2745C684D6547 CRC64;

Query Match 62.5%; Score 5; DB 2; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 NLDAE 7
|||||
Db 26 NLDAE 30

RESULT 33

Q8CKW2

ID Q8CKW2 PRELIMINARY; PRT; 55 AA.
AC Q8CKW2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical.
GN Y2748.
OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KIM5 / Biovar Mediaevalis;

RX MEDLINE=22137863; PubMed=12142430;
 RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
 RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
 RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
 RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
 RA Perry R.D.;
 RT "Genome sequence of Yersinia pestis KIM.";
 RL J. Bacteriol. 184:4601-4611(2002).
 DR EMBL; AE013877; AAM86301.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 55 AA; 5908 MW; FBC89479AC2DCB81 CRC64;

Query Match 62.5%; Score 5; DB 16; Length 55;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VNLDA 6
 |||||
 Db 9 VNLDA 13

RESULT 34

Q8WYE8

ID Q8WYE8 PRELIMINARY; PRT; 63 AA.
 AC Q8WYE8;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Dystrophin (Fragment).
 GN DMD.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Beggs A.H., Koenig M., Kunkel L.M.;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Worton R.G.;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA den Dunnen J.T.;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF213410; AAL61558.1; -.
 FT NON_TER 1 1
 FT NON_TER 63 63
 SQ SEQUENCE 63 AA; 7147 MW; C57D0C273C1E8A82 CRC64;

Query Match 62.5%; Score 5; DB 4; Length 63;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVNLD 5
 |||||

Db

18 EVNLD 22

RESULT 35

Q96X11

ID Q96X11 PRELIMINARY; PRT; 66 AA.
AC Q96X11;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mating type 2 protein (Fragment).
OS Phaeosphaeria avenaria f. sp. triticae.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
OC Pleosporales; Phaeosphaeriaceae; Phaeosphaeria.
OX NCBI_TaxID=54790;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC26370;
RA Dai Q., Cui K., Ueng P.P.;
RT "Mating type gene in Phaeosphaeria avenaria f. sp. triticae."
RL Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF358826; AAK51442.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR InterPro; IPR000910; HMG_12_box.
DR Pfam; PF00505; HMG_box; 1.
DR SMART; SM00398; HMG; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50118; HMG_BOX_2; 1.
FT NON_TER 1 1
FT NON_TER 66 66
SQ SEQUENCE 66 AA; 7936 MW; 532A84F37D334DBA CRC64;

Query Match 62.5%; Score 5; DB 3; Length 66;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 NLDAE 7

|||||

Db 35 NLDAE 39

RESULT 36

Q9TU51

ID Q9TU51 PRELIMINARY; PRT; 67 AA.
AC Q9TU51;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Regulator of G-protein signalling 16 (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99294626; PubMed=10364456;
 RA Panetta R., Guo Y., Magder S., Greenwood M.T.;
 RT "Regulators of G-protein signaling (RGS) 1 and 16 are induced in
 RT response to bacterial lipopolysaccharide and stimulate c-fos promoter
 RT expression.";
 RL Biochem. Biophys. Res. Commun. 259:550-556(1999).
 DR EMBL; AF139836; AAD53051.1; -.
 DR HSSP; P49799; 1AGR.
 DR GO; GO:0004871; F:signal transducer activity; IEA.
 DR InterPro; IPR000342; Regl_Gprotein.
 DR Pfam; PF00615; RGS; 1.
 DR ProDom; PD001580; Regl_Gprotein; 1.
 DR PROSITE; PS50132; RGS; 1.
 FT NON_TER 1 1
 FT NON_TER 67 67
 SQ SEQUENCE 67 AA; 7650 MW; 7335579D0FC83F83 CRC64;

Query Match 62.5%; Score 5; DB 6; Length 67;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVNLD 5
 |||||
 Db 34 EVNLD 38

RESULT 37

Q9IB55

ID Q9IB55 PRELIMINARY; PRT; 67 AA.
 AC Q9IB55;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Regulators of G protein signaling XRGSV (Fragment).
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20200091; PubMed=10733901;
 RA Saitoh O., Odagiri M., Masuho I., Nomoto S., Kinoshita N.;
 RT "Molecular cloning and characterization of Xenopus RGS5."
 RL Biochem. Biophys. Res. Commun. 270:34-39(2000).
 DR EMBL; AB038438; BAA95152.1; -.
 DR HSSP; P49799; 1AGR.
 DR GO; GO:0004871; F:signal transducer activity; IEA.
 DR InterPro; IPR000342; Regl_Gprotein.
 DR Pfam; PF00615; RGS; 1.
 DR PRINTS; PR01301; RGSPROTEIN.
 DR ProDom; PD001580; Regl_Gprotein; 1.
 DR PROSITE; PS50132; RGS; 1.
 FT NON_TER 1 1

FT NON_TER 67 67
SQ SEQUENCE 67 AA; 7906 MW; 74EF3B876826CECE CRC64;

Query Match 62.5%; Score 5; DB 13; Length 67;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLD 5
|
Db 34 EVNLD 38

RESULT 38

Q9IB58

ID Q9IB58 PRELIMINARY; PRT; 67 AA.
AC Q9IB58;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Regulators of G protein signaling XRGSI (Fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20200091; PubMed=10733901;
RA Saitoh O., Odagiri M., Masuho I., Nomoto S., Kinoshita N.;
RT "Molecular cloning and characterization of Xenopus RGS5.";
RL Biochem. Biophys. Res. Commun. 270:34-39(2000).
DR EMBL; AB038435; BAA95149.1; -.
DR HSSP; P49799; 1AGR.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR InterPro; IPR000342; Regl_Gprotein.
DR Pfam; PF00615; RGS; 1.
DR PRINTS; PR01301; RGSPROTEIN.
DR ProDom; PD001580; Regl_Gprotein; 1.
DR PROSITE; PS50132; RGS; 1.
FT NON_TER 1 1
FT NON_TER 67 67
SQ SEQUENCE 67 AA; 7716 MW; AA0ED8E536609E7B CRC64;

Query Match 62.5%; Score 5; DB 13; Length 67;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLD 5
|
Db 34 EVNLD 38

RESULT 39

Q8CN01

ID Q8CN01 PRELIMINARY; PRT; 68 AA.
AC Q8CN01;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Mercuric ion-binding protein.
 GN SE2120.
 OS Staphylococcus epidermidis.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1282;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 12228;
 RA Zhang Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Qin Z.,
 RA Chen Z., Wen Y.;
 RL Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AE016751; AAO05762.1; -.
 DR GO; GO:0005507; F:copper ion binding; IEA.
 DR GO; GO:0005375; F:copper ion transporter activity; IEA.
 DR GO; GO:0046872; F:metal ion binding; IEA.
 DR GO; GO:0006825; P:copper ion transport; IEA.
 DR GO; GO:0030001; P:metal ion transport; IEA.
 DR InterPro; IPR000428; Cu_bind.
 DR InterPro; IPR006122; Cu_bind_dom.
 DR InterPro; IPR006121; HeavyMe_transpt.
 DR InterPro; IPR006191; Metal_bind.
 DR Pfam; PF00403; HMA; 1.
 DR PRINTS; PR00944; CUEXPOR.
 DR TIGRFAMs; TIGR00003; TIGR00003; 1.
 DR PROSITE; PS01047; HMA_1; 1.
 DR PROSITE; PS50846; HMA_2; 1.
 KW Complete proteome.
 SQ SEQUENCE 68 AA; 7661 MW; F2BE2AC6992E36AA CRC64;

Query Match 62.5%; Score 5; DB 16; Length 68;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLD 5
 |||||
 Db 34 EVNLD 38

RESULT 40
 Q8NKU7

ID Q8NKU7 PRELIMINARY; PRT; 70 AA.
 AC Q8NKU7;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Membrane-bound NiFe hydrogenase.
 GN HYP1.
 OS Acidianus ambivalens (Desulfurolobus ambivalens).
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
 OC Acidianus.
 OX NCBI_TaxID=2283;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Lei 10;
 RA Laska S., Kletzin A.;

RT "Biochemical and Molecular analysis of the membrane-bound hydrogenase
RT of the hyperthermophilic and acidophilic archaeon Acidianus
RT ambivalens.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Lei 10;
RA Laska S.;
RL Thesis (2000), Institute of Microbiology and Genetics, Darmstadt.
DR EMBL; AJ320523; CAC86893.1; -.
SQ SEQUENCE 70 AA; 8189 MW; CFDDEC93F9FF7A2E CRC64;

Query Match 62.5%; Score 5; DB 1; Length 70;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVNLD 5
|||||
Db 43 EVNLD 47

Search completed: March 26, 2004, 15:35:45
Job time : 81 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 26, 2004, 15:30:32 ; Search time 10.5 Seconds
(without alignments)
39.672 Million cell updates/sec

Title: US-09-668-314C-71
Perfect score: 8
Sequence: 1 EVNLDAEF 8

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 141681 seqs, 52070155 residues

Word size : 0

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Listing first 1000 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		8						
Result	Query							
No.	Score	Match	Length	DB	ID	Description		
1	7	87.5	419	1	P47K_PSECL	P31521	pseudomonas	
2	6	75.0	295	1	DAP1_BACHD	Q9kc32	bacillus ha	
3	6	75.0	368	1	K1CR_XENLA	P08802	xenopus lae	
4	6	75.0	394	1	ALR2_BACSU	P94494	bacillus su	
5	6	75.0	621	1	MBHL_ALCHY	P33374	alcaligenes	
6	6	75.0	4639	1	DYHC_DROME	P37276	drosophila	
7	5	62.5	67	1	RGS3_RAT	P49797	rattus norv	
8	5	62.5	73	1	PHD_BPP1	Q06253	bacterioph	
9	5	62.5	90	1	EF1B_SULSO	Q64214	sulfolobus	
10	5	62.5	91	1	EF1B_PYRAB	Q9v2p6	pyrococcus	
11	5	62.5	91	1	EF1B_PYRFU	Q8tzm5	pyrococcus	
12	5	62.5	91	1	EF1B_SULTO	Q976h8	sulfolobus	
13	5	62.5	92	1	KM11_TRYBB	Q26773	trypanosoma	
14	5	62.5	92	1	KM11_TRYCR	Q9u6z1	trypanosoma	
15	5	62.5	119	1	ACPS_BACHD	Q9kfg1	bacillus ha	
16	5	62.5	126	1	PFD4_CAEEL	Q17435	caenorhabdi	
17	5	62.5	159	1	GREX_CHLTE	Q8kch5	chlorobium	

18	5	62.5	172	1	YFIR_ECOLI	P76597	escherichia
19	5	62.5	184	1	KAD1_ANASP	Q8ypj8	anabaena sp
20	5	62.5	185	1	TBP_METKA	Q8tx38	methanopyru
21	5	62.5	197	1	OM26_HAEIN	Q57483	haemophilus
22	5	62.5	197	1	YDB6_YEAST	Q12055	saccharomyc
23	5	62.5	202	1	GDIR_YEAST	Q12434	saccharomyc
24	5	62.5	205	1	RGS4_HUMAN	P49798	homo sapien
25	5	62.5	205	1	RGS4_MOUSE	O08899	mus musculu
26	5	62.5	205	1	RGS4_RAT	P49799	rattus norv
27	5	62.5	217	1	NFNB_ECOLI	P38489	escherichia
28	5	62.5	217	1	NFNB_SALTY	P15888	salmonella
29	5	62.5	225	1	MINC_PASMU	P57845	pasteurella
30	5	62.5	229	1	Y127_TREPA	O83164	treponema p
31	5	62.5	231	1	CTRA_CAUCR	Q45994	caulobacter
32	5	62.5	234	1	RL1_HELPJ	Q9zk21	helicobacte
33	5	62.5	235	1	RGS1_HUMAN	Q9ns28	homo sapien
34	5	62.5	239	1	NPD_RHOBA	Q7ufq9	rhodopirell
35	5	62.5	250	1	Y514_METJA	Q57934	methanococc
36	5	62.5	251	1	E1A_ADE41	P10542	human adeno
37	5	62.5	277	1	HEMK_BUCBP	Q89at0	buchnera ap
38	5	62.5	283	1	KPRS_METAC	Q8trk8	methanosarc
39	5	62.5	290	1	G3P_LACDT	P55070	lactarius d
40	5	62.5	291	1	G3P_BOLED	Q00301	boletus edu
41	5	62.5	304	1	G3P2_DROPS	O44104	drosophila
42	5	62.5	304	1	G3P2_DROSU	O44105	drosophila
43	5	62.5	305	1	YO31_STRGR	P36261	streptomyce
44	5	62.5	318	1	KDGT_XANAC	Q8pqi6	xanthomonas
45	5	62.5	330	1	VP19_HSVSA	Q01051	herpesvirus
46	5	62.5	332	1	G3P1_DROME	P07486	drosophila
47	5	62.5	332	1	G3P2_DROME	P07487	drosophila
48	5	62.5	332	1	G3P_DROHY	Q01597	drosophila
49	5	62.5	334	1	YMO1_RHIME	P49305	rhizobium m
50	5	62.5	337	1	G3P_OMPOL	Q8tfj2	omphalotus
51	5	62.5	337	1	G3P_PHACH	Q01982	phanerochae
52	5	62.5	337	1	G3P_USTMA	P09317	ustilago ma
53	5	62.5	337	1	MAT2_COCSA	Q9p445	cochliobolu
54	5	62.5	338	1	TRPD_DEIRA	Q9rtj5	deinococcus
55	5	62.5	339	1	G3P_CRYNE	Q9y8e9	cryptococcu
56	5	62.5	341	1	SYFA_MYCLE	Q9cc17	mycobacteri
57	5	62.5	344	1	PUR5_NEIMA	Q9jua2	neisseria m
58	5	62.5	344	1	PUR5_NEIMB	Q9jz80	neisseria m
59	5	62.5	350	1	YF98_METJA	Q58993	methanococc
60	5	62.5	351	1	RFBB_XANCP	P55295	xanthomonas
61	5	62.5	360	1	VIS_AGRVI	Q04554	agrobacteri
62	5	62.5	362	1	DCAM_IPOBA	Q9m6k1	ipomoea bat
63	5	62.5	362	1	DCAM_PHANI	Q96471	pharbitis n
64	5	62.5	363	1	LACK_AGRRD	Q01937	agrobacteri
65	5	62.5	366	1	KORA_METJA	Q57724	methanococc
66	5	62.5	371	1	DHA_MYCTU	P30234	mycobacteri
67	5	62.5	375	1	RF1_DEIRA	P56905	deinococcus
68	5	62.5	380	1	TPSA_CAEL	O77081	caenorhabdi
69	5	62.5	382	1	ALR_STAEP	Q8cnk7	staphylococ
70	5	62.5	388	1	ALR2_THETN	Q8r860	thermoanaer
71	5	62.5	390	1	FTSZ_STAAM	P45498	staphylococ
72	5	62.5	394	1	FTSZ_STAEP	Q8cpk4	staphylococ
73	5	62.5	395	1	PORA_PYRAB	Q9uyz4	pyrococcus
74	5	62.5	395	1	PORA_PYRHO	O73986	pyrococcus

75	5	62.5	396	1	PORA_PYRFU	Q51804	pyrococcus
76	5	62.5	397	1	DP3B_MYCSM	P52851	mycobacteri
77	5	62.5	399	1	DP3B_MYCLE	P46387	mycobacteri
78	5	62.5	399	1	DP3B_MYCPA	Q91716	mycobacteri
79	5	62.5	399	1	ISDF_TREPA	O83525	t ispd/ispf
80	5	62.5	402	1	DP3B_MYCBO	O33914	mycobacteri
81	5	62.5	402	1	DP3B_MYCTU	Q50790	mycobacteri
82	5	62.5	404	1	HISZ_ANASP	Q8yt12	anabaena sp
83	5	62.5	418	1	FTSZ_TREPA	O83405	treponema p
84	5	62.5	419	1	DNLI_ASFB7	P35970	african swi
85	5	62.5	419	1	DNLI_ASFM2	P26813	african swi
86	5	62.5	426	1	G6PI_HALN1	Q9hnq6	halobacteri
87	5	62.5	427	1	SAHH_HALN1	Q9hn50	halobacteri
88	5	62.5	434	1	PURA_CAEEEL	P91134	caenorhabdi
89	5	62.5	434	1	YRL4_CAEEEL	Q09413	caenorhabdi
90	5	62.5	436	1	PROA_PROMP	Q7v293	prochloroco
91	5	62.5	442	1	TRME_MYCPN	P75104	mycoplasma
92	5	62.5	448	1	MURD_PSEAE	Q9hvez9	pseudomonas
93	5	62.5	460	1	PYRD_ARATH	P32746	arabidopsis
94	5	62.5	462	1	FUMC_BACSU	P07343	bacillus su
95	5	62.5	469	1	TRIP_HUMAN	Q9bwf2	homo sapien
96	5	62.5	470	1	PUR1_METJA	Q57657	methanococc
97	5	62.5	470	1	TRIP_MOUSE	Q8vig6	mus musculu
98	5	62.5	472	1	UXAC_NOSPU	Q9khal	nostoc punc
99	5	62.5	492	1	MUE2_OCEIH	Q8cze4	oceanobacil
100	5	62.5	496	1	CWLB_BACSU	Q02114	bacillus su
101	5	62.5	497	1	GLYA_CHLMU	Q9pjw0	chlamydia m
102	5	62.5	497	1	GLYA_CHLTR	O84439	chlamydia t
103	5	62.5	499	1	BCHE_SYNY3	Q55373	synechocyst
104	5	62.5	500	1	GGPS_SYNP2	O65979	synechococc
105	5	62.5	509	1	C4A1_DROME	Q9vms9	drosophila
106	5	62.5	514	1	C4AA_DROME	Q9v7g5	drosophila
107	5	62.5	514	1	CBH2_SCHPO	O60108	schizosacch
108	5	62.5	518	1	LE12_METJA	Q58595	methanococc
109	5	62.5	519	1	RGS3_HUMAN	P49796	homo sapien
110	5	62.5	535	1	PYRG_CLOAB	Q97f61	clostridium
111	5	62.5	535	1	PYRG_CLOPE	Q8xib3	clostridium
112	5	62.5	568	1	RGS3_MOUSE	Q9dc04	mus musculu
113	5	62.5	576	1	DPEP_SOLTU	Q06801	solanum tub
114	5	62.5	580	1	GBA4_USTMA	P87035	ustilago ma
115	5	62.5	591	1	TYP_A_ECOLI	P32132	escherichia
116	5	62.5	607	1	TYP_A_ECOL6	Q9exn7	escherichia
117	5	62.5	660	1	FDL_DROME	Q8wsf3	drosophila
118	5	62.5	678	1	ABPP_RIPCL	Q27905	riptomus c
119	5	62.5	710	1	FIB1_ADEG1	Q64761	avian adeno
120	5	62.5	720	1	MCM5_SCHPO	P41389	schizosacch
121	5	62.5	725	1	VR2A_BPT4	P03690	bacterioph
122	5	62.5	727	1	MFP1_ARATH	Q9lw85	arabidopsis
123	5	62.5	738	1	MASZ_CORGL	P42450	corynebacte
124	5	62.5	748	1	MASZ_COREF	Q8fnb3	corynebacte
125	5	62.5	759	1	TRPG_SCHPO	Q92370	schizosacch
126	5	62.5	794	1	SC18_CANAL	P34732	candida alb
127	5	62.5	811	1	SYFB_OCEIH	Q8eph5	oceanobacil
128	5	62.5	829	1	DPOL_BPT5	P19822	bacterioph
129	5	62.5	845	1	CC47_YEAST	P38132	saccharomyc
130	5	62.5	863	1	PHSG_MYCTU	Q10639	mycobacteri
131	5	62.5	868	1	ACO2_SYNY3	P74582	synechocyst

132	5	62.5	874	1	SLAP_BACLI	P49052	bacillus li
133	5	62.5	882	1	HSS1_HUMAN	P52848	homo sapien
134	5	62.5	882	1	HSS1_RAT	Q02353	rattus norv
135	5	62.5	883	1	HSS2_HUMAN	P52849	homo sapien
136	5	62.5	883	1	HSS2_MOUSE	P52850	mus musculu
137	5	62.5	886	1	POL_FOAMV	P14350	human spuma
138	5	62.5	907	1	KCB2_RAT	Q63099	rattus norv
139	5	62.5	911	1	KCB2_HUMAN	Q92953	homo sapien
140	5	62.5	911	1	KCB2_RABIT	Q95111	oryctolagus
141	5	62.5	988	1	SYI_SYNY3	P73505	synechocyst
142	5	62.5	1017	1	A1A2_CHICK	P24797	gallus gall
143	5	62.5	1034	1	ITAV_CHICK	P26008	gallus gall
144	5	62.5	1049	1	ITA5_HUMAN	P08648	homo sapien
145	5	62.5	1053	1	ITA5_MOUSE	P11688	mus musculu
146	5	62.5	1072	1	ITA6_CHICK	P26007	gallus gall
147	5	62.5	1083	1	S127_HUMAN	Q9y666	homo sapien
148	5	62.5	1131	1	YPO4_CAEEL	P53015	caenorhabdi
149	5	62.5	1167	1	CARB_RHILO	Q98i87	rhizobium l
150	5	62.5	1178	1	RPOB_TREPA	O83269	treponema p
151	5	62.5	1271	1	RBMG_HUMAN	Q9upn6	homo sapien
152	5	62.5	1276	1	PMP6_CHLPN	Q9z899	chlamydia p
153	5	62.5	1405	1	RPC1_SCHPO	O94666	schizosacch
154	5	62.5	1483	1	YCDA_DROME	Q9vgw1	drosophila
155	5	62.5	1741	1	RPC1_GIALA	P25202	giardia lam
156	5	62.5	2696	1	NSD1_HUMAN	Q96173	homo sapien
157	5	62.5	3358	1	PGCV_MOUSE	Q62059	mus musculu
158	5	62.5	3562	1	PGCV_CHICK	Q90953	gallus gall
159	5	62.5	3660	1	DMD_CHICK	P11533	gallus gall
160	5	62.5	3678	1	DMD_MOUSE	P11531	mus musculu
161	5	62.5	3685	1	DMD_HUMAN	P11532	homo sapien
162	5	62.5	4725	1	DYHC_DICDI	P34036	dictyosteli
163	5	62.5	6758	1	RIAB_CVH22	Q05002	h replicase
164	5	62.5	8797	1	SNE1_HUMAN	Q8nf91	homo sapien
165	4	50.0	15	1	TERM_BPM2	P19897	bacteriopha
166	4	50.0	40	1	CSP4_STRMT	O33675	streptococc
167	4	50.0	53	1	Y525_METJA	Q57945	methanococc
168	4	50.0	54	1	VG87_BPMD2	O64268	mycobacteri
169	4	50.0	57	1	A4_URSMA	Q29149	ursus marit
170	4	50.0	58	1	A4_CANFA	Q28280	canis famil
171	4	50.0	58	1	A4_RABIT	Q28748	oryctolagus
172	4	50.0	58	1	A4_SHEEP	Q28757	ovis aries
173	4	50.0	59	1	A4_BOVIN	Q28053	bos taurus
174	4	50.0	59	1	YDBF_SCHPO	Q10365	schizosacch
175	4	50.0	59	1	YL61_ARCFU	O28121	archaeoglob
176	4	50.0	61	1	TBA4_MAIZE	P33626	zea mays (m
177	4	50.0	62	1	Y4DN_RHISN	P55413	rhizobium s
178	4	50.0	63	1	ANP1_AUSBR	P12100	austrolycic
179	4	50.0	63	1	YPH2_SYNP2	P32040	synechococc
180	4	50.0	64	1	VRAL_BPP22	P14113	bacteriopha
181	4	50.0	67	1	ATPE_SCHPO	P87316	schizosacch
182	4	50.0	69	1	DHAG_PIG	Q29228	sus scrofa
183	4	50.0	70	1	RPCX_YEAST	P40422	saccharomyc
184	4	50.0	70	1	UBIL_CAEBR	Q07371	caenorhabdi
185	4	50.0	70	1	V07K_PVX	P07698	potato viru
186	4	50.0	70	1	V07K_PVXX3	P17781	potato viru
187	4	50.0	71	1	YE35_METJA	Q58830	methanococc
188	4	50.0	72	1	RL15_BACLI	P35138	bacillus li

189	4	50.0	72	1	YA94_ARCFU	029171	archaeoglob
190	4	50.0	74	1	PSPB_ECOLI	P23854	escherichia
191	4	50.0	74	1	YD97_CAMJE	Q9pmr0	campylobact
192	4	50.0	75	1	TRY3_ECOLI	P05835	escherichia
193	4	50.0	75	1	Y14E_BPT4	P39508	bacteriopha
194	4	50.0	75	1	Y14E_BPT6	Q38168	bacteriopha
195	4	50.0	76	1	TATA_PASMU	Q9ckd3	pasteurella
196	4	50.0	77	1	RUXX_ARCFU	O29386	archaeoglob
197	4	50.0	79	1	C551_ECTHL	P38587	ectothiorho
198	4	50.0	79	1	VG68_BPML5	Q05282	mycobacteri
199	4	50.0	81	1	CFB5_HUMAN	Q9plf3	homo sapien
200	4	50.0	82	1	YNI1_FRAAL	P46041	frankia aln
201	4	50.0	83	1	EX7S_RHIME	Q92ri9	rhizobium m
202	4	50.0	84	1	UL24_HSVF	P13161	feline herp
203	4	50.0	85	1	GLR1_ECOLI	P00277	escherichia
204	4	50.0	88	1	ECLH_BOMMO	P25331	bombyx mori
205	4	50.0	89	1	BARS_BACAM	P11540	bacillus am
206	4	50.0	89	1	EAT1_ENTFA	Q9a101	enterococcu
207	4	50.0	89	1	EAT2_ENTFA	Q9a119	enterococcu
208	4	50.0	89	1	EATX_STRAG	Q936e0	streptococc
209	4	50.0	89	1	EATX_STRPY	Q57231	streptococc
210	4	50.0	89	1	TATA_HAEIN	P57046	haemophilus
211	4	50.0	89	1	YS22_BORBU	P70844	borrelia bu
212	4	50.0	91	1	EF1B_PYRHO	P58748	pyrococcus
213	4	50.0	91	1	RACC_ECOLI	P15033	escherichia
214	4	50.0	91	1	S112_PIG	P80310	sus scrofa
215	4	50.0	91	1	Y13F_BPT4	P39499	bacteriopha
216	4	50.0	92	1	CLP9_DROME	P82384	drosophila
217	4	50.0	96	1	RL15_STRSC	P43415	streptomyce
218	4	50.0	100	1	CBIN_ANASP	Q8yq90	anabaena sp
219	4	50.0	100	1	IM9B_MOUSE	Q9wv96	mus musculu
220	4	50.0	100	1	IM9B_RAT	Q9rlb1	rattus norv
221	4	50.0	102	1	CH10_STRAL	Q00769	streptomyce
222	4	50.0	102	1	CH10_STRCO	P40172	streptomyce
223	4	50.0	102	1	CMGC_BACHD	Q9k923	bacillus ha
224	4	50.0	103	1	CCK3_SYNY3	P73406	synechocyst
225	4	50.0	103	1	IM9B_HUMAN	Q9y5j6	homo sapien
226	4	50.0	103	1	S112_HUMAN	Q96fq6	homo sapien
227	4	50.0	103	1	VE7_HPV12	P36819	human papil
228	4	50.0	104	1	SR19_ARCFU	O29010	archaeoglob
229	4	50.0	105	1	FLHD_NITEU	Q82sd3	nitrosomona
230	4	50.0	105	1	HAL2_CANAL	P46594	candida alb
231	4	50.0	105	1	Y948_MYCTU	P71562	mycobacteri
232	4	50.0	106	1	FLIE_BACSU	P24502	bacillus su
233	4	50.0	107	1	FLHD_BORBR	Q44730	bordetella
234	4	50.0	107	1	FLHD_BORPA	Q7wab3	bordetella
235	4	50.0	107	1	FLHD_BORPE	Q7vza1	bordetella
236	4	50.0	107	1	T2AH_DROME	Q9w5b9	drosophila
237	4	50.0	107	1	THI2_CORNE	P07887	corynebacte
238	4	50.0	108	1	HUPN_AZOCH	Q43955	azotobacter
239	4	50.0	108	1	UL96_GPCMV	Q67669	guinea pig
240	4	50.0	109	1	THI2_SYNY3	P73263	synechocyst
241	4	50.0	109	1	YIR1_YEAST	P40440	saccharomyc
242	4	50.0	110	1	THI2_ANASP	P20857	anabaena sp
243	4	50.0	111	1	RL12_AERPE	Q9y9w9	aeropyrum p
244	4	50.0	112	1	PFD1_SCHPO	O14334	schizosacch
245	4	50.0	112	1	SPEH_ARCFU	O28663	archaeoglob

246	4	50.0	113	1	Y076_METJA	Q60383	methanococc
247	4	50.0	114	1	Y364_METJA	Q57810	methanococc
248	4	50.0	114	1	YOAB_ECOLI	P76258	escherichia
249	4	50.0	115	1	R18E_HALMA	P12733	haloarcula
250	4	50.0	115	1	VATG_NEUCR	P78713	neurospora
251	4	50.0	116	1	NGF_NAJAT	P21377	naja atra (
252	4	50.0	116	1	NGF_NAJNA	P01140	naja naja (
253	4	50.0	116	1	YE94_HAEIN	O05071	haemophilus
254	4	50.0	117	1	R18E_HALN1	Q9v2w0	halobacteri
255	4	50.0	119	1	SY24_HUMAN	O00175	homo sapien
256	4	50.0	119	1	YGL1_STRVR	P19434	streptomyce
257	4	50.0	120	1	R18E_AERPE	Q9yb51	aeropyrum p
258	4	50.0	120	1	RBFA_CHLTE	Q8kft0	chlorobium
259	4	50.0	120	1	Y4NI_RHISN	P55581	rhizobium s
260	4	50.0	121	1	R18E_METJA	P54022	methanococc
261	4	50.0	121	1	RK14_ODOSI	P49552	odontella s
262	4	50.0	121	1	RL5_SOLME	P93779	solanum mel
263	4	50.0	121	1	RS13_ENTFA	P59754	enterococcu
264	4	50.0	121	1	RS13_LISMO	Q927n1	listeria mo
265	4	50.0	121	1	RS13_STRAS	Q8e7r9	streptococc
266	4	50.0	121	1	RS13_STRMU	Q8ds35	streptococc
267	4	50.0	121	1	RS13_STRPN	Q97st9	streptococc
268	4	50.0	123	1	AZUP_PARDE	P80649	paracoccus
269	4	50.0	123	1	RS13_CLOTE	Q890q7	clostridium
270	4	50.0	124	1	PRIB_HAEDU	Q7vmd6	haemophilus
271	4	50.0	124	1	TSP_MOUSE	P13438	mus musculu
272	4	50.0	124	1	Y670_PASMU	Q9cmy0	pasteurella
273	4	50.0	125	1	DHSC_COXBU	P51055	coxiella bu
274	4	50.0	125	1	YHEN_PASHA	P95509	pasteurella
275	4	50.0	125	1	YM07_PARTE	P15608	paramecium
276	4	50.0	126	1	CD59_RAT	P27274	rattus norv
277	4	50.0	126	1	GCSH_BACTN	Q8a4s8	bacteroides
278	4	50.0	126	1	Y576_HAEIN	P44762	haemophilus
279	4	50.0	127	1	VG41_HAEIN	P44235	haemophilus
280	4	50.0	129	1	DHSC_ECOLI	P10446	escherichia
281	4	50.0	129	1	DHSC_SALTY	Q8xg40	salmonella
282	4	50.0	129	1	GCSH_SHEON	Q8eiq7	shewanella
283	4	50.0	129	1	NIFA_AZOCH	P56269	azotobacter
284	4	50.0	131	1	FABA_BOVIN	P48035	bos taurus
285	4	50.0	131	1	SDIS_PSEPU	P07445	pseudomonas
286	4	50.0	131	1	VG11_BPML5	Q05296	mycobacteri
287	4	50.0	132	1	AMP1_ALLCE	Q41258	allium cepa
288	4	50.0	132	1	FLSA_PSEAE	O33422	pseudomonas
289	4	50.0	132	1	GCSH_MYCLE	O32920	mycobacteri
290	4	50.0	133	1	Y044_BORBU	O51073	borrelia bu
291	4	50.0	134	1	GCSH_MYCTU	Q50607	mycobacteri
292	4	50.0	134	1	RS16_BRUME	Q8yj59	brucella me
293	4	50.0	136	1	RNK_ECOLI	P40679	escherichia
294	4	50.0	139	1	FLIJ_CAUCR	O05529	caulobacter
295	4	50.0	139	1	RISB_METTH	O27443	methanobact
296	4	50.0	140	1	Y138_CAMJE	Q9piy9	campylobact
297	4	50.0	144	1	RUVX_RALSO	Q8y1l4	ralstonia s
298	4	50.0	144	1	Y013_RICPR	Q9zed0	rickettsia
299	4	50.0	145	1	AZUP_PARPEN	P80401	paracoccus
300	4	50.0	145	1	NINB_BPP22	Q38662	bacterioph
301	4	50.0	145	1	YAF4_SCHPO	Q09858	schizosacch
302	4	50.0	145	1	YPH2_MYCCA	P45614	mycoplasma

303	4	50.0	146	1	NINB_ECOL6	Q9xjq1	escherichia
304	4	50.0	146	1	NINB_LAMBD	P03765	bacterioph
305	4	50.0	146	1	R27B_ARATH	Q9lr33	arabidopsis
306	4	50.0	146	1	R27C_ARATH	P49637	arabidopsis
307	4	50.0	146	1	RL15_BACSU	P19946	bacillus su
308	4	50.0	146	1	RL15_STAAM	O06445	staphylococ
309	4	50.0	146	1	Y101_HAEIN	P43942	haemophilus
310	4	50.0	146	1	Y619_DEIRA	Q9rwp7	deinococcus
311	4	50.0	146	1	YN21_DEIRA	Q9rs06	deinococcus
312	4	50.0	147	1	DEF1_CLOPE	Q8xjl2	clostridium
313	4	50.0	147	1	G10_CAEEL	P34313	caenorhabdi
314	4	50.0	147	1	RL2A_HUMAN	P46776	homo sapien
315	4	50.0	147	1	RL2A_MOUSE	P14115	mus musculu
316	4	50.0	147	1	RL2A_RAT	P18445	rattus norv
317	4	50.0	148	1	R28A_SCHPO	P36585	schizosacch
318	4	50.0	148	1	R28B_SCHPO	P57728	schizosacch
319	4	50.0	149	1	RECX_AMYMD	Q9rev5	amycolatops
320	4	50.0	149	1	Y282_METJA	Q57730	methanococc
321	4	50.0	150	1	RL15_MICLU	P33101	micrococcus
322	4	50.0	150	1	SP0A_BACCE	P52930	bacillus ce
323	4	50.0	150	1	TPCB_HOMAM	P29291	homarus ame
324	4	50.0	151	1	MRAZ_HAEIN	P45056	haemophilus
325	4	50.0	151	1	MRAZ_PSESM	Q87wx6	pseudomonas
326	4	50.0	151	1	PFD5_ARATH	P57742	arabidopsis
327	4	50.0	151	1	RL15_STRCO	P46787	streptomyce
328	4	50.0	151	1	TCPR_VIBCH	P29483	vibrio chol
329	4	50.0	151	1	Y4JR_RHISN	P55518	rhizobium s
330	4	50.0	152	1	MRAZ_ECOL6	Q8x9z3	escherichia
331	4	50.0	152	1	MRAZ_ECOLI	P22186	escherichia
332	4	50.0	152	1	MRAZ_SALTI	Q8z9h5	salmonella
333	4	50.0	152	1	MRAZ_SALTY	Q8zru9	salmonella
334	4	50.0	152	1	MRAZ_YERPE	Q8zif8	yersinia pe
335	4	50.0	152	1	TRI3_HUMAN	Q15649	homo sapien
336	4	50.0	153	1	HIS3_RHILO	Q981q5	rhizobium l
337	4	50.0	153	1	NRDI_MYCPN	P75460	mycoplasma
338	4	50.0	154	1	YM64_ARCFU	O28020	archaeoglob
339	4	50.0	155	1	LACB_MACGI	P11944	macropus gi
340	4	50.0	156	1	PHNG_RHIME	Q52984	rhizobium m
341	4	50.0	156	1	SOXR_PSEAE	Q51506	pseudomonas
342	4	50.0	156	1	YF60_HAEIN	P44253	haemophilus
343	4	50.0	157	1	ISPF_LISIN	Q92f39	listeria in
344	4	50.0	157	1	ISPF_LISMO	Q8yab4	listeria mo
345	4	50.0	157	1	RRAA_MYCLE	Q9cdd2	mycobacteri
346	4	50.0	159	1	NIFX_RHOCA	P19078	rhodobacter
347	4	50.0	160	1	FLAV_CLOSA	P18855	clostridium
348	4	50.0	160	1	ISPF_FUSNN	Q8r6e7	fusobacteri
349	4	50.0	160	1	MOAC_ECOLI	P30747	escherichia
350	4	50.0	160	1	MOAC_HAEIN	P45310	haemophilus
351	4	50.0	160	1	SSB_CHLPN	Q9z8f7	chlamydia p
352	4	50.0	160	1	Y178_HAEIN	P43961	haemophilus
353	4	50.0	160	1	Y881_ENTFA	Q837g1	enterococcu
354	4	50.0	161	1	FARP_ASCSU	P41854	a fmrfamide
355	4	50.0	161	1	SSB_CHLCV	Q823k0	chlamydophi
356	4	50.0	161	1	Y088_BRUME	Q8yjj5	brucella me
357	4	50.0	161	1	YJ79_BRUSU	Q8fya6	brucella su
358	4	50.0	161	1	YVGO_BACSU	O32211	bacillus su
359	4	50.0	162	1	DYR_HALVO	P15093	halobacteri

360	4	50.0	164	1	PHEA_SYN1	P20778	synechocyst
361	4	50.0	164	1	YN87_BACHD	Q9kaa3	bacillus ha
362	4	50.0	164	1	YT83_RHIME	P29953	rhizobium m
363	4	50.0	165	1	LB21_ARATH	Q9srl8	arabidopsis
364	4	50.0	166	1	IL3_RAT	P04823	rattus norv
365	4	50.0	166	1	TPX_HELPJ	Q9zke7	helicobacte
366	4	50.0	166	1	TPX_HELPY	O25151	helicobacte
367	4	50.0	167	1	DYR_ENTFC	P00380	enterococcu
368	4	50.0	167	1	RT25_DROME	Q9vy28	drosophila
369	4	50.0	167	1	TCTP_MEDSA	P28014	medicago sa
370	4	50.0	168	1	GREB_PSEAE	Q9hzy5	pseudomonas
371	4	50.0	168	1	LED2_METJA	Q58673	methanococc
372	4	50.0	168	1	NUE2_RHIME	P56910	rhizobium m
373	4	50.0	168	1	TCTP_ORYSA	P35681	oryza sativ
374	4	50.0	168	1	TCTP_SOYBN	Q944t2	glycine max
375	4	50.0	168	1	YXKA_BACSU	P55185	bacillus su
376	4	50.0	170	1	BMAE_ECOLI	P05818	escherichia
377	4	50.0	170	1	IF3_BACHD	Q9k867	bacillus ha
378	4	50.0	170	1	LED1_METKA	Q8tx94	methanopyru
379	4	50.0	171	1	TOXS_VIBPA	Q05939	vibrio para
380	4	50.0	172	1	LECA_PLEWA	Q02988	pleurodeles
381	4	50.0	172	1	Y074_NPVOP	O10327	orgyia pseu
382	4	50.0	172	1	YH74_METTH	O27802	methanobact
383	4	50.0	173	1	DEF_BUCAI	P57563	buchnera ap
384	4	50.0	173	1	ESMD_DROME	Q01071	drosophila
385	4	50.0	173	1	HSLV_AGRT5	Q8uj88	agrobacteri
386	4	50.0	174	1	CRAB_ANAPL	Q05557	anas platyr
387	4	50.0	174	1	CRAB_CHICK	Q05713	gallus gall
388	4	50.0	174	1	LACB_MACEU	Q29614	macropus eu
389	4	50.0	174	1	STA_ECOLI	P13018	escherichia
390	4	50.0	175	1	CRAB_BOVIN	P02510	bos taurus
391	4	50.0	175	1	CRAB_HUMAN	P02511	homo sapien
392	4	50.0	175	1	CRAB_MESAU	P05811	mesocricetu
393	4	50.0	175	1	CRAB_MOUSE	P23927	mus musculu
394	4	50.0	175	1	CRAB_RABIT	P41316	oryctolagus
395	4	50.0	175	1	CRAB_RAT	P23928	rattus norv
396	4	50.0	175	1	PYRE_HALN1	Q9hng2	halobacteri
397	4	50.0	175	1	Y013_RICCN	Q92jq4	rickettsia
398	4	50.0	175	1	YH1E_ECOLI	P29688	escherichia
399	4	50.0	176	1	ARA1_ARAHY	P20780	arachis hyp
400	4	50.0	176	1	HSLV_RHIME	Q92ta9	rhizobium m
401	4	50.0	176	1	YWY1_CAEEL	Q11088	caenorhabdi
402	4	50.0	178	1	BDH_BOVIN	Q02337	bos taurus
403	4	50.0	178	1	I17B_MESAU	Q9eqi6	mesocricetu
404	4	50.0	179	1	KPTA_FUSNN	Q8r5n7	fusobacteri
405	4	50.0	179	1	YFGI_ECOLI	P76573	escherichia
406	4	50.0	180	1	BST2_HUMAN	Q10589	homo sapien
407	4	50.0	180	1	I17B_HUMAN	Q9uhf5	homo sapien
408	4	50.0	180	1	I17B_MOUSE	Q9qxt6	mus musculu
409	4	50.0	180	1	RE15_SCHPO	Q09094	schizosacch
410	4	50.0	181	1	YAEQ_ECOLI	P52100	escherichia
411	4	50.0	181	1	YG34_MYCPN	P75163	mycoplasma
412	4	50.0	182	1	ATPF_GUITH	O78477	guillardia
413	4	50.0	183	1	DUT_STRCO	O54134	streptomyce
414	4	50.0	183	1	Y212_BOTCI	P56739	botrytis ci
415	4	50.0	184	1	PAAD_METJA	Q57566	methanococc
416	4	50.0	185	1	COME_METTH	O27275	methanobact

417	4	50.0	186	1	ARDH_LEIDO	Q05885	leishmania
418	4	50.0	186	1	DEF_CHLCV	Q823u4	chlamydophi
419	4	50.0	186	1	KAD_SYN6	Q24706	synechococc
420	4	50.0	187	1	O204_ARATH	P82805	arabidopsis
421	4	50.0	187	1	SIGW_BACSU	Q45585	bacillus su
422	4	50.0	188	1	EFPL_XANCP	Q8p9m3	xanthomonas
423	4	50.0	188	1	EFPL_XYLFT	Q87c43	xylella fas
424	4	50.0	188	1	Y020_YERPE	Q8zjr9	yersinia pe
425	4	50.0	188	1	Y4AQ_RHISN	P55364	rhizobium s
426	4	50.0	189	1	TBP_THECE	Q56253	thermococcu
427	4	50.0	190	1	BCT7_SHEEP	P50415	ovis aries
428	4	50.0	190	1	GP38_BPSP1	Q48394	bacterioph
429	4	50.0	190	1	RS9A_SCHPO	Q09757	schizosacch
430	4	50.0	190	1	TBP_PYRKO	Q52366	pyrococcus
431	4	50.0	191	1	HUGN_DROME	Q9vg55	drosophila
432	4	50.0	191	1	RS9B_SCHPO	O59675	schizosacch
433	4	50.0	191	1	SP0A_BACPU	P52933	bacillus pu
434	4	50.0	191	1	TXLA_SYN7	P35088	synechococc
435	4	50.0	192	1	CD3E_SHEEP	P29328	ovis aries
436	4	50.0	193	1	RNH2_RICPR	Q9zdw3	rickettsia
437	4	50.0	193	1	RPSH_PSEAE	Q06198	pseudomonas
438	4	50.0	194	1	GRPE_BACHD	Q9kd73	bacillus ha
439	4	50.0	194	1	HIS7_CHLTE	Q8kef4	chlorobium
440	4	50.0	194	1	RS9B_YEAST	P05755	saccharomyc
441	4	50.0	194	1	RUVA_XYLFA	Q9pc77	xylella fas
442	4	50.0	194	1	RUVA_XYLFT	Q87d02	xylella fas
443	4	50.0	195	1	IND1_HUMAN	P37290	homo sapien
444	4	50.0	195	1	Y061_CAUCR	Q9ac08	caulobacter
445	4	50.0	196	1	ELI_PEA	P11432	pisum sativ
446	4	50.0	196	1	RS9A_YEAST	O13516	saccharomyc
447	4	50.0	197	1	GPX4_HUMAN	P36969	homo sapien
448	4	50.0	197	1	GPX4_PIG	P36968	sus scrofa
449	4	50.0	197	1	NUOC_RICPR	Q9zdh3	rickettsia
450	4	50.0	197	1	PSD9_CAEEL	Q10920	caenorhabdi
451	4	50.0	197	1	RUVA_CLOHI	Q9znj6	clostridium
452	4	50.0	197	1	TBP_SULAC	Q9uwn7	sulfolobus
453	4	50.0	198	1	TBP_SULSH	Q55031	sulfolobus
454	4	50.0	198	1	TBP_SULSO	P58178	sulfolobus
455	4	50.0	198	1	TBP_SULTO	Q97lv3	sulfolobus
456	4	50.0	199	1	UREG_HELPJ	Q9zmz7	helicobacte
457	4	50.0	199	1	UREG_HELPY	Q09066	helicobacte
458	4	50.0	200	1	ISPZ_BRUME	Q8yjf3	brucella me
459	4	50.0	200	1	ISPZ_BRUSU	P59363	brucella su
460	4	50.0	200	1	LEUD_SYNY3	P74207	synechocyst
461	4	50.0	200	1	TBP1_ARATH	P28147	arabidopsis
462	4	50.0	200	1	TBP1_MAIZE	P50158	zea mays (m
463	4	50.0	200	1	TBP2_ARATH	P28148	arabidopsis
464	4	50.0	200	1	TBP2_MAIZE	P50159	zea mays (m
465	4	50.0	200	1	TBP_MESCR	P48511	mesembryant
466	4	50.0	200	1	TBP_SOLTU	P26357	solanum tub
467	4	50.0	200	1	TBP_SOYBN	Q42808	glycine max
468	4	50.0	200	1	TBP_TOBAC	P93348	nicotiana t
469	4	50.0	201	1	HIS7_METKA	P58879	methanopyru
470	4	50.0	201	1	TBP2_WHEAT	Q02879	triticum ae
471	4	50.0	201	1	YD84_THEVO	Q978n1	thermoplasm
472	4	50.0	202	1	CD3E_CANFA	P27597	canis famil
473	4	50.0	202	1	LEXA_PSECL	Q8kt78	pseudomonas

474	4	50.0	202	1	Y038_MYCLE	Q50191	mycobacteri
475	4	50.0	203	1	RS4_CHLTE	P59129	chlorobium
476	4	50.0	203	1	YBM4_YEAST	P38068	saccharomyc
477	4	50.0	203	1	YKV4_YEAST	P36036	saccharomyc
478	4	50.0	204	1	CLP1_ANASP	Q8yxh5	anabaena sp
479	4	50.0	204	1	QOX3_BACSU	P34958	bacillus su
480	4	50.0	204	1	TRPF_OCEIH	Q8esu3	oceanobacil
481	4	50.0	204	1	YM09_PARTE	P15610	paramecium
482	4	50.0	204	1	YTUB_ERWHE	Q47826	erwinia her
483	4	50.0	206	1	RL25_THETH	P56930	thermus the
484	4	50.0	206	1	T2D8_YEAST	Q12030	saccharomyc
485	4	50.0	207	1	COAE_XYLFA	Q9pai2	xylella fas
486	4	50.0	207	1	COAE_XYLFT	Q87aa7	xylella fas
487	4	50.0	207	1	GIDB_NEIMA	Q9jx38	neisseria m
488	4	50.0	207	1	GIDB_NEIMB	Q9klg3	neisseria m
489	4	50.0	207	1	HIS7_AZOBR	P18787	azospirillu
490	4	50.0	207	1	JAG_BACHD	Q9rca6	bacillus ha
491	4	50.0	207	1	OGG1_METJA	Q58134	methanococc
492	4	50.0	208	1	YLIJ_ECOLI	P75805	escherichia
493	4	50.0	209	1	ATI3_VACCV	P21117	vaccinia vi
494	4	50.0	209	1	HIS7_ANASP	Q05068	anabaena sp
495	4	50.0	209	1	PROQ_HAEIN	P44286	haemophilus
496	4	50.0	209	1	RHEB_YEAST	P25378	saccharomyc
497	4	50.0	209	1	RL3_BACHD	Q9z914	bacillus ha
498	4	50.0	209	1	VG40_BPPH8	P14817	bacterioph
499	4	50.0	209	1	VS10_ROTBS	P34718	bovine rota
500	4	50.0	209	1	YNU1_SHIFL	P29770	shigella fl
501	4	50.0	210	1	HCC1_HUMAN	P82979	homo sapien
502	4	50.0	210	1	HCC1_MOUSE	Q9dlj3	mus musculu
503	4	50.0	210	1	SPOA_BACCI	P52931	bacillus ci
504	4	50.0	210	1	VS10_ROTPO	P36358	porcine rot
505	4	50.0	211	1	SODF_ACIAM	Q9p913	acidianus a
506	4	50.0	211	1	UREG_ACTPL	O54424	actinobacil
507	4	50.0	212	1	IL6_CERTO	P46650	cercocoebus
508	4	50.0	212	1	IL6_HUMAN	P05231	homo sapien
509	4	50.0	212	1	IL6_MACFA	P79341	macaca fasc
510	4	50.0	212	1	IL6_MACMU	P51494	macaca mula
511	4	50.0	212	1	SPOA_BACME	P52932	bacillus me
512	4	50.0	212	1	SPOA_BREPA	P52929	brevibacill
513	4	50.0	212	1	TAL_BACHD	Q9k6e4	bacillus ha
514	4	50.0	212	1	VS10_ROTHC	Q00682	human rotav
515	4	50.0	213	1	TM21_FUGRU	Q90515	fugu rubrip
516	4	50.0	214	1	KTHY_BRUME	Q8yh15	brucella me
517	4	50.0	214	1	KTHY_BRUSU	Q8g0u3	brucella su
518	4	50.0	214	1	SPOA_BACAN	P52928	bacillus an
519	4	50.0	214	1	YHQ5_YEAST	P38815	saccharomyc
520	4	50.0	215	1	FUCA_ECOLI	P11550	escherichia
521	4	50.0	215	1	TAL_CLOAB	Q97jd9	clostridium
522	4	50.0	215	1	UCRI_YEAST	P08067	saccharomyc
523	4	50.0	216	1	ALL7_LEPDS	Q9ulg2	lepidoglyph
524	4	50.0	216	1	LOLB_XYLFA	Q9pa74	xylella fas
525	4	50.0	216	1	Y726_METJA	Q58136	methanococc
526	4	50.0	217	1	BIOS_RHIME	O08250	rhizobium m
527	4	50.0	217	1	TAL_AQUAE	O66520	aquifex aeo
528	4	50.0	218	1	ATTE_DROME	Q9v751	drosophila
529	4	50.0	218	1	HRF1_NPVLD	Q90165	lymantria d
530	4	50.0	218	1	LOLB_XYLFT	Q87a20	xylella fas

531	4	50.0	218	1	RISA_PHOLE	Q01993	photobacter
532	4	50.0	218	1	RR3_EUGGR	P19169	euglena gra
533	4	50.0	218	1	TRKA_METJA	Q58505	methanococc
534	4	50.0	219	1	CD28_BOVIN	Q28071	bos taurus
535	4	50.0	219	1	RLUA_HAEIN	P44782	haemophilus
536	4	50.0	219	1	RLUA_PASMU	Q9ck02	pasteurella
537	4	50.0	219	1	VG36_BPT2	P07066	bacterioph
538	4	50.0	219	1	YOPE_YEREN	P31492	yersinia en
539	4	50.0	219	1	YOPE_YERPE	P31493	yersinia pe
540	4	50.0	219	1	YOPE_YERPS	P08008	yersinia ps
541	4	50.0	220	1	GCH1_YERPE	Q8zg15	yersinia pe
542	4	50.0	220	1	RK21_ARATH	P51412	arabidopsis
543	4	50.0	221	1	CD28_RABIT	P42069	oryctolagus
544	4	50.0	221	1	Y4EO_RHISN	P55438	rhizobium s
545	4	50.0	222	1	HUTG_KLEAE	P19452	klebsiella
546	4	50.0	222	1	NANE_OCEIH	Q8emp6	oceanobacil
547	4	50.0	222	1	YF88_MYCTU	O06602	mycobacteri
548	4	50.0	222	1	YY66_MYCTU	O06331	mycobacteri
549	4	50.0	224	1	ATTA_DROME	P45884	drosophila
550	4	50.0	224	1	COMB_METJA	Q58540	methanococc
551	4	50.0	224	1	GUNX_CLOTM	P15329	clostridium
552	4	50.0	224	1	IAPL_ASFB7	Q65138	african swi
553	4	50.0	224	1	IAPL_ASFC3	O11451	african swi
554	4	50.0	224	1	IAPL_ASFCH	O12407	african swi
555	4	50.0	224	1	IAPL_ASFM1	O11452	african swi
556	4	50.0	224	1	ISPZ_RHILO	Q98eb3	rhizobium l
557	4	50.0	224	1	LPRP_MYCBO	P59987	mycobacteri
558	4	50.0	224	1	LPRP_MYCTU	P71548	mycobacteri
559	4	50.0	224	1	UREG_MYCTU	P50051	mycobacteri
560	4	50.0	225	1	GCH3_SULTO	Q975m4	sulfolobus
561	4	50.0	225	1	RT26_DROME	Q9vvn2	drosophila
562	4	50.0	225	1	UREG_HAEIN	P44396	haemophilus
563	4	50.0	226	1	CLP2_SYNY3	Q59993	synechocyst
564	4	50.0	226	1	COMB_METHH	O27250	methanobact
565	4	50.0	226	1	IF3B_ARATH	Q9sza3	arabidopsis
566	4	50.0	226	1	IF3B_ORYSA	Q94hf1	oryza sativ
567	4	50.0	226	1	YM74_YEAST	Q05024	saccharomyc
568	4	50.0	227	1	VATE_SCHPO	O13687	schizosacch
569	4	50.0	227	1	YP85_DEIRA	Q9rra9	deinococcus
570	4	50.0	228	1	PSDA_YEAST	P50086	saccharomyc
571	4	50.0	229	1	CLP1_SYNEL	Q8dli2	synechococc
572	4	50.0	230	1	DP3E_RICCN	Q92gl1	rickettsia
573	4	50.0	230	1	SFMC_ECOLI	P77249	escherichia
574	4	50.0	231	1	ISPF_ARATH	Q9cak8	arabidopsis
575	4	50.0	231	1	TBP_SCHPO	P17871	schizosacch
576	4	50.0	232	1	CLP2_ANASP	Q8yqx8	anabaena sp
577	4	50.0	232	1	YHJY_ECOLI	P37663	escherichia
578	4	50.0	233	1	ATE_VIBPA	Q87qy2	vibrio para
579	4	50.0	233	1	LOLD_ECOLI	P75957	escherichia
580	4	50.0	233	1	NAGB_ENTFA	P59687	enterococcu
581	4	50.0	233	1	NAGB_STRPN	Q97ql6	streptococc
582	4	50.0	233	1	SERA_ENTHI	P21138	entamoeba h
583	4	50.0	233	1	TBP1_WHEAT	P26356	triticum ae
584	4	50.0	233	1	TNFA_MARMO	O35734	marmota mon
585	4	50.0	234	1	TAL_DEIRA	Q9rup6	deinococcus
586	4	50.0	234	1	TFD2_ALCEU	P42428	alcaligenes
587	4	50.0	234	1	TNFA_CAVPO	P51435	cavia porce

588	4	50.0	235	1	NAGB_LACLA	Q9cfa8	lactococcus
589	4	50.0	235	1	NAGB_STRR6	Q8dpa1	streptococc
590	4	50.0	235	1	TNFA_MOUSE	P06804	mus musculu
591	4	50.0	235	1	TNFA_PERLE	P36939	peromyscus
592	4	50.0	235	1	TNFA_RAT	P16599	rattus norv
593	4	50.0	236	1	CYH2_BACSU	O06737	bacillus su
594	4	50.0	236	1	ISPF_CATRO	Q9m4w3	catharanthu
595	4	50.0	236	1	PHOU_XYLFA	Q9pbj9	xylella fas
596	4	50.0	236	1	TRAR_RHISN	P55407	rhizobium s
597	4	50.0	237	1	GPH_CAUCR	Q9a5z2	caulobacter
598	4	50.0	237	1	NAGB_LACPL	Q88zs6	lactobacill
599	4	50.0	237	1	SFSA_PSEPK	Q88dx7	pseudomonas
600	4	50.0	237	1	YM50_YEAST	Q03246	saccharomyc
601	4	50.0	238	1	ATPO_ARATH	Q96251	arabidopsis
602	4	50.0	238	1	HIS4_METVA	P05324	methanococc
603	4	50.0	238	1	IAPL_ASFM2	O11453	african swi
604	4	50.0	238	1	RIBB_ARCFU	O28173	archaeoglob
605	4	50.0	238	1	TBP_CANAL	O43133	candida alb
606	4	50.0	238	1	Y035_TREPA	O83078	treponema p
607	4	50.0	238	1	YCDB_LACLA	Q9cix4	lactococcus
608	4	50.0	239	1	HIS4_CLOAB	Q97kh9	clostridium
609	4	50.0	240	1	BAER_ECOLI	P30846	escherichia
610	4	50.0	240	1	HEM4_METJA	Q58401	methanococc
611	4	50.0	240	1	PHOU_XYLEFT	Q87c87	xylella fas
612	4	50.0	240	1	SP2B_BOVIN	P79125	bos taurus
613	4	50.0	240	1	ZEAA_MAIZE	P06678	zea mays (m
614	4	50.0	241	1	HFB1_HAEIN	P35757	haemophilus
615	4	50.0	241	1	PUR7_BACSU	P12046	bacillus su
616	4	50.0	241	1	YC34_METJA	Q58631	methanococc
617	4	50.0	241	1	YEEN_SALTI	Q8z0y7	salmonella
618	4	50.0	241	1	YEEN_SALTY	Q8zk08	salmonella
619	4	50.0	242	1	6PGL_PSEPU	Q9ev79	pseudomonas
620	4	50.0	242	1	NAGB_BACSU	O35000	bacillus su
621	4	50.0	242	1	YDO5_SCHPO	O13725	schizosacch
622	4	50.0	243	1	CYSH_ECO57	Q8x7u3	escherichia
623	4	50.0	243	1	CYSH_ECOL6	Q8fei9	escherichia
624	4	50.0	243	1	CYSH_ECOLI	P17854	escherichia
625	4	50.0	243	1	CYSH_SHIFL	Q7ubt0	shigella fl
626	4	50.0	243	1	IPTZ_AGRT5	P58758	agrobacteri
627	4	50.0	243	1	IPTZ_AGRT7	P06524	agrobacteri
628	4	50.0	243	1	NPD_SHEON	Q8efn2	shewanella
629	4	50.0	244	1	MOAC_PYRAE	Q8zyf8	pyrobaculum
630	4	50.0	244	1	NOG4_RHIME	P06235	rhizobium m
631	4	50.0	244	1	P29_MYCPN	P75370	mycoplasma
632	4	50.0	244	1	YKL4_CAEEL	P42171	caenorhabdi
633	4	50.0	245	1	MCT1_SHEEP	P80931	ovis aries
634	4	50.0	245	1	NODG_RHIME	P06234	rhizobium m
635	4	50.0	245	1	NODG_RHIS3	P72332	rhizobium s
636	4	50.0	245	1	P29_MYCGE	P47532	mycoplasma
637	4	50.0	245	1	PCN1_SULOH	P57762	sulfurispha
638	4	50.0	245	1	PCN1_SULTO	Q975n2	sulfolobus
639	4	50.0	245	1	RLUA_VIBCH	Q9kp71	vibrio chol
640	4	50.0	245	1	TRUA_ZYMMO	Q9req0	zymomonas m
641	4	50.0	245	1	Y303_HAEIN	P44627	haemophilus
642	4	50.0	245	1	YM29_MYCTU	Q10513	mycobacteri
643	4	50.0	246	1	PDXJ_PSEPK	Q88my2	pseudomonas
644	4	50.0	246	1	PDXJ_PSESM	Q87xg4	pseudomonas

645	4	50.0	246	1	THIM_AGRT5	Q8uas9	agrobacteri
646	4	50.0	246	1	Y980_PASMU	Q9cm61	pasteurella
647	4	50.0	246	1	YM95_CLOAB	Q97gs1	clostridium
648	4	50.0	247	1	COBK_PSEDE	P21920	pseudomonas
649	4	50.0	247	1	KDSB_ECO57	Q8xdg6	escherichia
650	4	50.0	247	1	KDSB_ECOL6	Q8fja9	escherichia
651	4	50.0	247	1	KDSB_ECOLI	P04951	escherichia
652	4	50.0	247	1	KDSB_SALTI	Q8z800	salmonella
653	4	50.0	247	1	KDSB_SALTY	Q8zqc0	salmonella
654	4	50.0	247	1	MCT8_MOUSE	P43430	mus musculu
655	4	50.0	247	1	RS2_FUSNN	Q8rih7	fusobacteri
656	4	50.0	247	1	YK55_YERPE	Q8zeu8	yersinia pe
657	4	50.0	247	1	YL12_PSEAE	Q9i203	pseudomonas
658	4	50.0	248	1	GRL2_RAT	Q06606	rattus norv
659	4	50.0	248	1	HIS4_BRAJA	Q89wm5	bradyrhizob
660	4	50.0	248	1	MCT8_RAT	P97594	rattus norv
661	4	50.0	248	1	PDXJ_PSEAE	Q9i5g5	pseudomonas
662	4	50.0	248	1	YEGW_ECOLI	P76420	escherichia
663	4	50.0	248	1	YO32_SHEON	Q8eef0	shewanella
664	4	50.0	249	1	HCDS_XANP2	Q56841	xanthobacte
665	4	50.0	249	1	PSA7_CICAR	Q9sxul	cicer ariet
666	4	50.0	250	1	PSD8_CAEEL	Q23449	caenorhabdi
667	4	50.0	250	1	Y035_METJA	Q60350	methanococc
668	4	50.0	250	1	YM19_MYCTU	Q10405	mycobacteri
669	4	50.0	251	1	GPMA_TREPA	P96121	treponema p
670	4	50.0	251	1	Y484_MYCTU	Q11150	mycobacteri
671	4	50.0	252	1	RS3_PHYS2	O66098	phytoplasma
672	4	50.0	252	1	YH76_COREF	Q8fpk2	corynebacte
673	4	50.0	253	1	DP3E_PASMU	Q9cpe0	pasteurella
674	4	50.0	253	1	MOX1_MOUSE	P32442	mus musculu
675	4	50.0	253	1	PCRB_METJA	Q58647	methanococc
676	4	50.0	253	1	PSB3_STRA3	Q8e313	streptococc
677	4	50.0	253	1	YK86_XANCP	Q8p8z2	xanthomonas
678	4	50.0	254	1	CBYC_ALCEU	P40119	alcaligenes
679	4	50.0	254	1	CBYP_ALCEU	Q04541	alcaligenes
680	4	50.0	254	1	MOX1_HUMAN	P50221	homo sapien
681	4	50.0	254	1	PDHR_ECOLI	P06957	escherichia
682	4	50.0	254	1	PDHR_SALTY	Q914h9	salmonella
683	4	50.0	254	1	PSTB_DEIRA	Q9ryz3	deinococcus
684	4	50.0	254	1	PT22_YEAST	P10355	saccharomyc
685	4	50.0	254	1	TPIS_ARATH	P48491	arabidopsis
686	4	50.0	255	1	BRAF_PSEAE	P21629	pseudomonas
687	4	50.0	255	1	COX3_THEAN	Q37679	theileria a
688	4	50.0	255	1	DAPB_STRMU	Q8dul9	streptococc
689	4	50.0	255	1	MINC_RALSO	Q8xu30	ralstonia s
690	4	50.0	255	1	STX6_HUMAN	O43752	homo sapien
691	4	50.0	255	1	STX6_RAT	Q63635	rattus norv
692	4	50.0	255	1	YABD_BACSU	P37545	bacillus su
693	4	50.0	255	1	YG08_THETN	Q8r9j9	thermoanaer
694	4	50.0	256	1	CU02_HUMAN	O43822	homo sapien
695	4	50.0	256	1	DP3E_HAEIN	P43745	haemophilus
696	4	50.0	256	1	HIS4_SYNY3	P74561	synechocyst
697	4	50.0	256	1	PTMA_CAMCO	Q45983	campylobact
698	4	50.0	256	1	TPI1_RHILO	Q98me7	rhizobium l
699	4	50.0	256	1	VATD_YEAST	P32610	saccharomyc
700	4	50.0	257	1	AP1B_MOUSE	Q8c7n7	mus musculu
701	4	50.0	257	1	ARGB_YERPE	Q8za87	yersinia pe

702	4	50.0	257	1	DCH_THAAR	087873	thauera aro
703	4	50.0	257	1	HIS4_ANASP	Q8ynq6	anabaena sp
704	4	50.0	257	1	Y123_PYRAB	Q9v2f1	pyrococcus
705	4	50.0	257	1	Y125_PYRHO	O57865	pyrococcus
706	4	50.0	257	1	YAAA_SALTI	Q8z9r5	salmonella
707	4	50.0	258	1	AP1C_MOUSE	Q9dcz9	mus musculus
708	4	50.0	258	1	UL24_VZVD	P09288	varicella-z
709	4	50.0	258	1	Y504_VIBPA	Q87sc0	vibrio para
710	4	50.0	258	1	Y9H7_PSEPK	Q88e89	pseudomonas
711	4	50.0	258	1	YURA_MYXXA	P25970	myxococcus
712	4	50.0	259	1	ALDC_KLETE	Q04518	klebsiella
713	4	50.0	259	1	PGH1_BOVIN	O62664	bos taurus
714	4	50.0	259	1	PSA7_LYCES	O24030	lycopersico
715	4	50.0	259	1	SP0A_BACST	P52934	bacillus st
716	4	50.0	259	1	UPKB_BOVIN	P38573	bos taurus
717	4	50.0	259	1	YC89_PSEPK	Q88nc3	pseudomonas
718	4	50.0	259	1	YGFM_ECOLI	Q46813	escherichia
719	4	50.0	260	1	ALDC_ENTAE	P05361	enterobacte
720	4	50.0	260	1	CCG6_HUMAN	Q9bxt2	homo sapien
721	4	50.0	260	1	CCG6_MOUSE	Q8vhw3	mus musculus
722	4	50.0	260	1	CCG6_RAT	Q8vhw7	rattus norv
723	4	50.0	260	1	DCK_RAT	P48769	rattus norv
724	4	50.0	260	1	TNF5_MOUSE	P27548	mus musculus
725	4	50.0	260	1	YD69_AQUAE	O67381	aquifex aeo
726	4	50.0	260	1	YG38_METJA	Q59032	methanococc
727	4	50.0	261	1	CODY_STRAT	P59387	streptococc
728	4	50.0	261	1	SUHB_NEIMA	Q9ju03	neisseria m
729	4	50.0	261	1	SUHB_NEIMB	Q9jz07	neisseria m
730	4	50.0	261	1	YH86_SYNY3	P73335	synechocyst
731	4	50.0	262	1	ARGB_VIBCH	Q9knt7	vibrio chol
732	4	50.0	262	1	NAGB_BACAA	Q81mh5	bacillus an
733	4	50.0	262	1	NAGB_BACCR	Q819d1	bacillus ce
734	4	50.0	262	1	PLC1_CAEEL	Q93841	caenorhabdi
735	4	50.0	263	1	ARGB_VIBPA	Q87156	vibrio para
736	4	50.0	263	1	GP3D_CHLTR	P10557	chlamydia t
737	4	50.0	263	1	THIM_STAAM	Q99sg5	staphylococ
738	4	50.0	264	1	GP3D_CHLMU	Q46439	chlamydia m
739	4	50.0	264	1	MOV_P_TOML	P03584	tomato mosa
740	4	50.0	264	1	MOV_P_TOML2	P29800	tomato mosa
741	4	50.0	264	1	MOV_P_TOMLA	P29799	tomato mosa
742	4	50.0	264	1	MOV_P_TOMS1	Q9yjq9	tomato mosa
743	4	50.0	264	1	SP0A_BACCR	P52935	bacillus ce
744	4	50.0	264	1	TRUA_YERPE	Q8zd27	yersinia pe
745	4	50.0	265	1	CYSH_RHIME	P56891	rhizobium m
746	4	50.0	265	1	HEM4_MOUSE	P51163	mus musculus
747	4	50.0	265	1	SR21_SARPE	P24491	sarcophaga
748	4	50.0	265	1	YGL7_YEAST	P53133	saccharomyc
749	4	50.0	266	1	LEF1_NPVAC	P41417	autographa
750	4	50.0	266	1	NAGB_ECOL6	Q8fjx7	escherichia
751	4	50.0	266	1	NAGB_ECOLI	P09375	escherichia
752	4	50.0	266	1	NAGB_SALTI	Q8z8g0	salmonella
753	4	50.0	266	1	NAGB_SALTY	Q8zqx7	salmonella
754	4	50.0	266	1	NAGB_SHIFL	P59688	shigella fl
755	4	50.0	266	1	NAGB_VIBPA	Q87k60	vibrio para
756	4	50.0	266	1	NAGB_YERPE	Q8zdel	yersinia pe
757	4	50.0	266	1	TERM_BPB03	Q37883	bacterioph
758	4	50.0	266	1	TERM_BPNF	P06812	bacterioph

759	THIM_STAAM	1	266	50.0	4
760	Y209_METJA	1	266	50.0	4
761	DKGB_ECO57	1	267	50.0	4
762	DKGB_ECOLI	1	267	50.0	4
763	DKGB_SALTI	1	267	50.0	4
764	DKGB_SALTY	1	267	50.0	4
765	NAGB_PASMU	1	267	50.0	4
766	PPN2_LISMO	1	267	50.0	4
767	SP0A_BACSU	1	267	50.0	4
768	MOVE_TMV	1	268	50.0	4
769	MOVE_TMV	1	268	50.0	4
770	MOVE_TMVKR	1	268	50.0	4
771	MOVE_TMVM	1	268	50.0	4
772	MOVE_TMVR	1	268	50.0	4
773	TBP_EMENT	1	268	50.0	4
774	TRPC_BRUME	1	268	50.0	4
775	YAU6_SCHPO	1	268	50.0	4
776	YC24_PSEPK	1	268	50.0	4
777	RFAZ_SALTY	1	269	50.0	4
778	SAPF_HAEIN	1	269	50.0	4
779	T2S1_STRFI	1	269	50.0	4
780	THID_HELPJ	1	269	50.0	4
781	TRUA_HAEIN	1	269	50.0	4
782	ETFB_MEGEL	1	270	50.0	4
783	MODE_AZOVI	1	270	50.0	4
784	NAGB_BACTN	1	270	50.0	4
785	NAGB_HAEIN	1	270	50.0	4
786	NFI_CHICK	1	270	50.0	4
787	RBTB_KLEAE	1	270	50.0	4
788	THID_HELPY	1	270	50.0	4
789	TRUA_ECOL6	1	270	50.0	4
790	TRUA_ECOLI	1	270	50.0	4
791	TRUA_SALTI	1	270	50.0	4
792	TRUA_SALTY	1	270	50.0	4
793	Y701_ARCFU	1	270	50.0	4
794	YA73_METJA	1	270	50.0	4
795	KPR2_ARCFU	1	271	50.0	4
796	TRUB_CAMJE	1	272	50.0	4
797	UL24_HSVEI	1	272	50.0	4
798	UL24_HSVE4	1	272	50.0	4
799	UL24_HSVEB	1	272	50.0	4
800	MPT4_YEAST	1	273	50.0	4
801	NIFH_METMA	1	273	50.0	4
802	VE08_VACCV	1	273	50.0	4
803	VE08_VACCV	1	273	50.0	4
804	VE08_VARV	1	273	50.0	4
805	Y818_RHITO	1	273	50.0	4
806	YI52_HALHA	1	273	50.0	4
807	NUCE_STRPN	1	274	50.0	4
808	PANB_AERPE	1	274	50.0	4
809	Y772_TREPA	1	274	50.0	4
810	YE03_MYCTU	1	274	50.0	4
811	YE06_YEAST	1	274	50.0	4
812	YFDQ_ECOLI	1	274	50.0	4
813	YKV2_CAEEL	1	274	50.0	4
814	IF2A_PYRAB	1	275	50.0	4
815	IF2A_PYRFU	1	275	50.0	4
Q8nvh4	staphylococ	1	266	50.0	4
Q57662	methanococc	1	267	50.0	4
Q8x727	escherichia	1	267	50.0	4
P30863	escherichia	1	267	50.0	4
Q8z988	salmonella	1	267	50.0	4
Q8zrm7	salmonella	1	267	50.0	4
Q9cmf4	pasteurella	1	267	50.0	4
Q92bc2	listeria mo	1	267	50.0	4
P06534	bacillus su	1	267	50.0	4
P03583	tobacco mos	1	268	50.0	4
O91275	tobacco mos	1	268	50.0	4
P30737	tobacco mos	1	268	50.0	4
P03582	tobacco mos	1	268	50.0	4
Q98746	tobacco mos	1	268	50.0	4
Q12731	emerella	1	268	50.0	4
Q8yhft8	brucella me	1	268	50.0	4
Q10162	schizosacch	1	268	50.0	4
P43037	pseudomonas	1	269	50.0	4
P26473	salmonella	1	269	50.0	4
P45289	haemophilus	1	269	50.0	4
O52512	streptomyce	1	269	50.0	4
Q9z100	helicobacte	1	269	50.0	4
P45291	haemophilus	1	269	50.0	4
O85691	megasphaera	1	270	50.0	4
P37733	azotobacter	1	270	50.0	4
Q8a094	bacteroides	1	270	50.0	4
P44538	haemophilus	1	270	50.0	4
P35608	gallus gall	1	270	50.0	4
P07760	klebsiella	1	270	50.0	4
O25515	helicobacte	1	270	50.0	4
Q8xcr2	escherichia	1	270	50.0	4
P07649	escherichia	1	270	50.0	4
Q8z500	salmonella	1	270	50.0	4
Q8znb9	salmonella	1	270	50.0	4
O29557	archaeoglob	1	270	50.0	4
Q58473	methanococc	1	270	50.0	4
O28853	archaeoglob	1	271	50.0	4
Q9pnj2	campylobact	1	272	50.0	4
P09314	equine herp	1	272	50.0	4
P24432	equine herp	1	272	50.0	4
P28927	equine herp	1	272	50.0	4
P39015	saccharomyc	1	273	50.0	4
Q8pyy0	methanosarc	1	273	50.0	4
P21049	vaccinia vi	1	273	50.0	4
P23372	vaccinia vi	1	273	50.0	4
P33820	variola vir	1	273	50.0	4
Q98dy5	rhizobium l	1	273	50.0	4
P04137	halobacteri	1	273	50.0	4
Q03158	streptococc	1	274	50.0	4
Q9ye97	aeropyrum p	1	274	50.0	4
O83751	treponema p	1	274	50.0	4
P71671	mycobacteri	1	274	50.0	4
P40072	saccharomyc	1	274	50.0	4
P76513	escherichia	1	274	50.0	4
P34324	caenorhabdi	1	274	50.0	4
Q9v0e4	pyrococcus	1	275	50.0	4
Q8ulr5	pyrococcus	1	275	50.0	4

816	IF2A_PYRHO	1	275	50.0	4
817	YC77_YEAST	1	275	50.0	4
818	RR43_HUMAN	1	276	50.0	4
819	RR43_MOUSE	1	276	50.0	4
820	SP0A_CLOIN	1	277	50.0	4
821	VNST_CVBQ	1	277	50.0	4
822	COT6_HUMAN	1	278	50.0	4
823	Y541_CHLPN	1	278	50.0	4
824	ATPY_YEAST	1	279	50.0	4
825	FADR_VIBCH	1	279	50.0	4
826	RFA2_SCHPO	1	279	50.0	4
827	TONB_HAEDU	1	279	50.0	4
828	SACY_BACSU	1	280	50.0	4
829	Y466_HAEIN	1	280	50.0	4
830	YBB0_YEAST	1	280	50.0	4
831	EX9_ECOLI	1	281	50.0	4
832	HIS1_CORGL	1	281	50.0	4
833	Y709_XYLFY	1	281	50.0	4
834	YE94_XYLFY	1	281	50.0	4
835	PANC_SXNY3	1	282	50.0	4
836	YMA8_CAEEL	1	282	50.0	4
837	Y43C_MYCPN	1	283	50.0	4
838	FLAL_VIBPA	1	284	50.0	4
839	RP32_BUCAL	1	284	50.0	4
840	URED_BORPE	1	284	50.0	4
841	RP32_BUCAP	1	285	50.0	4
842	ATL4_ASPEU	1	286	50.0	4
843	CHVD_AGRU	1	286	50.0	4
844	ID11_CLABR	1	287	50.0	4
845	UL24_ILTVT	1	287	50.0	4
846	PSTB_MYCPE	1	288	50.0	4
847	REPA_ECOLI	1	288	50.0	4
848	SECF_AQUAE	1	288	50.0	4
849	YG53_YEAST	1	288	50.0	4
850	AROE_BRUME	1	289	50.0	4
851	AROE_BRUSU	1	289	50.0	4
852	G3P_AMAMU	1	289	50.0	4
853	PAI_PROVU	1	289	50.0	4
854	PRMA_CHLTE	1	289	50.0	4
855	WR38_ARATH	1	289	50.0	4
856	SGCG_HUMAN	1	290	50.0	4
857	SGCG_MESAU	1	290	50.0	4
858	SGCG_MOUSE	1	290	50.0	4
859	CORC_VIBCH	1	291	50.0	4
860	DACX_STRSK	1	291	50.0	4
861	KPRS_METKA	1	291	50.0	4
862	TYE7_YEAST	1	291	50.0	4
863	AMYD_THETU	1	292	50.0	4
864	CITG_ECO57	1	292	50.0	4
865	CITG_ECOLI	1	292	50.0	4
866	DHI1_SHEEP	1	292	50.0	4
867	KPP2_RHOSH	1	292	50.0	4
868	PER2_CUCSA	1	292	50.0	4
869	YJ58_YEAST	1	292	50.0	4
870	ADH1_ZEALU	1	293	50.0	4
871	ALF1_PORGI	1	293	50.0	4
872	BLAC_RHOCA	1	293	50.0	4
058655	PYROCOCUS				
P25627	SACCHAROMYC				
Q96b26	HOMO SAPIEN				
Q9d753	MUS MUSCULU				
P52939	CLOSTRIDIUM				
P18517	BOVINE CORO				
Q9bx19	HOMO SAPIEN				
Q92811	CHLAMYDIA P				
P18496	SACCHAROMYC				
Q9kqu8	VIBRIO CHOL				
Q92373	SCHIZOSACCH				
O51810	HAEMOPHILUS				
P15401	BACILLUS SU				
P44000	HAEMOPHILUS				
P32788	SACCHAROMYC				
P38506	ESCHERICHIA				
Q92472	CORYNEBACTE				
Q87dh6	XYLLA FAS				
Q9pd85	XYLLA FAS				
Q55073	SYNECHOCYST				
P34453	CAENORHABDI				
P75153	MYCOPLASMA				
Q03473	VIBRIO PARA				
O05385	BUCHERA AP				
O06704	BORDETELLA				
Q8ka76	BUCHERA AP				
O60024	ASPERGILLUS				
P12622	AGROBACTERI				
Q39472	CLARKIA BRE				
P23986	INFECTION				
Q8eu1	MYCOPLASMA				
P05833	ESCHERICHIA				
O67536	AQUILEX AEO				
P50091	SACCHAROMYC				
Q8ye20	BRUCELLA ME				
Q8fy21	BRUCELLA SU				
P55071	AMANITA MUS				
P37447	PROTEUS VUL				
Q8kg70	CHLOROBIIUM				
Q8gwf1	ARABIDOPSIS				
Q13326	HOMO SAPIEN				
O08597	MESOCRICETU				
P82348	MUS MUSCULU				
Q9kte3	VIBRIO CHOL				
P39042	STREPTOMYCE				
Q8tut6	METHANOPYRU				
P33122	SACCHAROMYC				
P37730	THERMOANAER				
P58161	ESCHERICHIA				
P77231	ESCHERICHIA				
P51975	OVIS ARLES				
P23010	RHODOBACTER				
P19135	CUCUMIS SAT				
P47133	SACCHAROMYC				
Q07264	ZEALUXURIA				
P60053	PORPHYROMON				
P14171	RHODOBACTER				

Q9s3p9	vibratio angu	MOTY_VIBAN	1	293	50.0	4	873
Q38772	antirrhinum	CC2A_ANTMA	1	294	50.0	4	874
Q41639	vigna aconit	CD22_VIGAC	1	294	50.0	4	875
P52389	vigna unguis	CD22_VIGUN	1	294	50.0	4	876
P24751	eschlerichia	G3P1_ESCVU	1	294	50.0	4	877
P24163	enterobacte	G3P_ENTAE	1	294	50.0	4	878
P24749	eschlerichia	G3P_ESCBL	1	294	50.0	4	879
P24750	eschlerichia	G3P_ESCHE	1	294	50.0	4	880
P24166	serratia ma	G3P_SERMA	1	294	50.0	4	881
P24753	serratia od	G3P_SEROD	1	294	50.0	4	882
P52691	synchococc	LTRA_SYNPF	1	294	50.0	4	883
P18813	enterobacte	MALK_ENTAE	1	294	50.0	4	884
P24489	sarcophaga	SR22_SARPE	1	294	50.0	4	885
P24490	sarcophaga	SR23_SARPE	1	294	50.0	4	886
P14667	sarcophaga	SR2_SARPE	1	294	50.0	4	887
Q8kiy0	synchococc	TRUB_SYNPF	1	294	50.0	4	888
Q07159	staphylococ	ALFL_STACA	1	295	50.0	4	889
Q97gh8	clostridium	ARGB_CLOAB	1	295	50.0	4	890
Q8pux3	methanosarc	KPRS_METMA	1	295	50.0	4	891
Q9pnj6	campylobact	PYRB_CAMJE	1	295	50.0	4	892
Q47141	eschlerichia	HGAR_ECOLI	1	296	50.0	4	893
O28273	archaeoglob	MOAA_ARCFU	1	296	50.0	4	894
P97532	rattus norv	THTM_RAT	1	296	50.0	4	895
Q39099	arabidopsis	XTH4_ARATH	1	296	50.0	4	896
P23572	drosohilla	CD22_DROME	1	297	50.0	4	897
Q8zyw7	pyrobaculum	HEM3_PYRAE	1	297	50.0	4	898
P11072	eschlerichia	LIT_ECOLI	1	297	50.0	4	899
Q9cxf0	pasteurella	XERD_PASMU	1	297	50.0	4	900
P39021	xenopus lae	MOX2_XENTL	1	298	50.0	4	901
Q8xbj2	eschlerichia	YFEU_ECO57	1	298	50.0	4	902
Q8fjb0	eschlerichia	YFEU_ECOL6	1	298	50.0	4	903
P76535	eschlerichia	YFEU_ECOLI	1	298	50.0	4	904
Q83qn4	shigella fl	YFEU_SHIFL	1	298	50.0	4	905
P32142	eschlerichia	YIHU_ECOLI	1	298	50.0	4	906
Q8thj9	methanosarc	ARGB_METAC	1	299	50.0	4	907
P11122	pseudomonas	BRHC_PSEPA	1	299	50.0	4	908
Q59199	bacteroides	G3P_BACFR	1	299	50.0	4	909
Q8zfx4	yersinia pe	HIS1_YERPE	1	299	50.0	4	910
P22939	eschlerichia	ISPA_ECOLI	1	299	50.0	4	911
Q50713	mycobacteri	YX13_MYCTU	1	299	50.0	4	912
P74309	synchocyst	ALFL_SYNY3	1	300	50.0	4	913
P75157	mycoplasma	Y43E_MYCPN	1	300	50.0	4	914
Q84424	vibratio vuln	Y8E1_VIBVU	1	300	50.0	4	915
Q87fd6	vibratio para	YLE3_VIBPA	1	300	50.0	4	916
Q06309	leishmania	CRK1_LEIME	1	301	50.0	4	917
P96172	vibratio sp.	OTC_VIBS2	1	301	50.0	4	918
P49227	arabidopsis	RL5_ARATH	1	301	50.0	4	919
O59953	neurospora	RL5_NEUCR	1	301	50.0	4	920
Q9hpa4	halobacteri	TRUB_HALT1	1	301	50.0	4	921
Q9p153	chlamydia m	XERD_CHLMU	1	301	50.0	4	922
O27083	methanobact	COBK_METTH	1	302	50.0	4	923
Q9pqs5	ureaplasma	ENG3_UREPA	1	302	50.0	4	924
Q88my4	pseudomonas	ERA_PSEPK	1	302	50.0	4	925
P37931	pseudomonas	HRPS_PSESY	1	302	50.0	4	926
Q9pgr1	xyella fas	TRUB_XYLEFA	1	302	50.0	4	927
Q87ev2	xyella fas	TRUB_XYLEFT	1	302	50.0	4	928
Q7nee9	gloeobacter	ARGB_GLOVI	1	303	50.0	4	929

930	4	50.0	303	1	G3P_KLEFN
931	4	50.0	303	1	MOX2_HUMAN
932	4	50.0	303	1	MOX2_MOUSE
933	4	50.0	303	1	MOX2_RAT
934	4	50.0	303	1	PYRD_PYRAB
935	4	50.0	303	1	VMP_SOCMV
936	4	50.0	304	1	VIRA_VIBAN
937	4	50.0	304	1	YDEQ_ECOLI
938	4	50.0	305	1	TRXB_SPIBA
939	4	50.0	306	1	FLIH_BORBU
940	4	50.0	306	1	RS1_SYNPE
941	4	50.0	307	1	BLAC_MYCTU
942	4	50.0	307	1	TBP_BOMMO
943	4	50.0	308	1	CAPA_ARATH
944	4	50.0	308	1	RPNB_SCHPO
945	4	50.0	308	1	TRUB_DEIRA
946	4	50.0	309	1	COAA_LACPL
947	4	50.0	309	1	TRUB_YEREN
948	4	50.0	310	1	ARCC_HAEIN
949	4	50.0	311	1	7B4C_PSESP
950	4	50.0	311	1	ALSB_ECOLI
951	4	50.0	311	1	MIAA_HELPY
952	4	50.0	311	1	BPAC_STRPY
953	4	50.0	311	1	RADA_METHH
954	4	50.0	311	1	TRXB_CHLPN
955	4	50.0	311	1	UPPI_MOUSE
956	4	50.0	311	1	YDAO_ECOLI
957	4	50.0	312	1	KIPF_ECOLI
958	4	50.0	312	1	MIAA_HELPJ
959	4	50.0	312	1	PANE_LACLA
960	4	50.0	312	1	TRUB_HAEIN
961	4	50.0	312	1	TRXB_CHIMU
962	4	50.0	312	1	TRXB_CHLTR
963	4	50.0	313	1	HUTG_SALTI
964	4	50.0	313	1	HUTG_SALTY
965	4	50.0	313	1	META_VIBCH
966	4	50.0	313	1	PYRB_AGR75
967	4	50.0	313	1	PYRB_RHIME
968	4	50.0	313	1	Y763_TREPA
969	4	50.0	313	1	YDAO_HAEIN
970	4	50.0	313	1	YK89_ARCFU
971	4	50.0	314	1	HUTG_COREF
972	4	50.0	314	1	TRUB_VIBPA
973	4	50.0	314	1	TRUB_VIBVU
974	4	50.0	315	1	ACCA_HAEIN
975	4	50.0	315	1	ENGQ_PORGI
976	4	50.0	316	1	ARGC_XANAC
977	4	50.0	316	1	GSHB_XANAC
978	4	50.0	316	1	GSHB_XANCP
979	4	50.0	316	1	KHSE_PSEAE
980	4	50.0	316	1	RIBC_BACSU
981	4	50.0	316	1	TAL_VIBCH
982	4	50.0	316	1	YI51_PYRFU
983	4	50.0	317	1	GSHB_CAUCR
984	4	50.0	317	1	HUTG_BORBR
985	4	50.0	317	1	PRMA_STRAS
986	4	50.0	317	1	PRMA_STRAS
987	4	50.0	317	1	PRMA_STRAS
988	4	50.0	317	1	PRMA_STRAS
989	4	50.0	317	1	PRMA_STRAS
990	4	50.0	317	1	PRMA_STRAS
991	4	50.0	317	1	PRMA_STRAS
992	4	50.0	317	1	PRMA_STRAS
993	4	50.0	317	1	PRMA_STRAS
994	4	50.0	317	1	PRMA_STRAS
995	4	50.0	317	1	PRMA_STRAS
996	4	50.0	317	1	PRMA_STRAS
997	4	50.0	317	1	PRMA_STRAS
998	4	50.0	317	1	PRMA_STRAS
999	4	50.0	317	1	PRMA_STRAS
1000	4	50.0	317	1	PRMA_STRAS

987	4	50.0	317	1	RFAC_SALTY	P26469	salmonella
988	4	50.0	317	1	VEAA_BPP22	Q03544	bacteriopha
989	4	50.0	317	1	YI87_AQUAE	O67728	aquifex aeo
990	4	50.0	318	1	KHSE_METGL	O32378	methylobaci
991	4	50.0	318	1	SOLR_CLOAB	P33746	clostridium
992	4	50.0	318	1	TRB1_YEAST	P29509	saccharomyc
993	4	50.0	318	1	TRXB_HAEIN	P43788	haemophilus
994	4	50.0	318	1	TRXB_VIBCH	Q9kss4	vibrio chol
995	4	50.0	319	1	HI81_ARCFU	O28277	archaeoglob
996	4	50.0	319	1	YXEB_BACSU	P54941	bacillus su
997	4	50.0	320	1	PTA_MYCGE	P47541	mycoplasma
998	4	50.0	320	1	PTA_MYCPN	P75359	mycoplasma
999	4	50.0	320	1	PU72_CAUCR	Q9a3g2	caulobacter
1000	4	50.0	320	1	TRXB_COXBU	P39916	coxiella bu

ALIGNMENTS

RESULT 1

P47K_PSECL

ID P47K_PSECL STANDARD; PRT; 419 AA.
AC P31521;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 47 kDa protein (P47K).
OS Pseudomonas chlororaphis (Pseudomonas aureofaciens).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=333;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B23;
RX MEDLINE=91193202; PubMed=2013568;
RA Nishiyama M., Horinouchi S., Kobayashi M., Nagasawa T., Yamada H.,
RA Beppu T.;
RT "Cloning and characterization of genes responsible for metabolism of
RT nitrile compounds from Pseudomonas chlororaphis B23.";
RL J. Bacteriol. 173:2465-2472(1991).
CC -!- FUNCTION: THE PRESENCE OF P47K IS CRITICAL FOR THE EXPRESSION
CC OF THE NITRILE HYDRATASE GENES. MAY STABILIZE OR ACTIVATE THE
CC NITRILE HYDRATASE PROTEINS.
CC -----
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CC -----
DR EMBL; D90216; BAA14247.1; -.
DR PIR; D42725; D42725.
DR InterPro; IPR003495; CobW.
DR Pfam; PF02492; cobW; 1.
SQ SEQUENCE 419 AA; 46666 MW; FF5113800E27FF0C CRC64;

Query Match 87.5%; Score 7; DB 1; Length 419;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAE 7
|||||||
Db 48 EVNLDAE 54

RESULT 2

DAP1_BACHD

ID DAP1_BACHD STANDARD; PRT; 295 AA.
AC Q9KC32;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Dihydrodipicolinate synthase 1 (EC 4.2.1.52) (DHDPS 1).
GN DAP1 OR BH1742.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hiramata C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331(2000).
CC -!- CATALYTIC ACTIVITY: L-aspartate 4-semialdehyde + pyruvate =
CC dihydrodipicolinate + 2 H(2)O.
CC -!- PATHWAY: Biosynthesis of diaminopimelate and lysine from aspartate
CC semialdehyde; first step.
CC -!- SUBUNIT: Homotetramer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the DHDPS family.
CC -----
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CC -----
DR EMBL; AP001513; BAB05461.1; -.
DR PIR; F83867; F83867.
DR HSSP; P05640; 1DHP.
DR HAMAP; MF_00418; -, 1.
DR InterPro; IPR005263; DapA.
DR InterPro; IPR002220; DHDPS.
DR Pfam; PF00701; DHDPS; 1.
DR PRINTS; PR00146; DHPICSNTHASE.
DR ProDom; PD001859; DHDPS; 1.

DR TIGRFAMs; TIGR00674; dapA; 1.
 DR PROSITE; PS00665; DHDPS_1; 1.
 DR PROSITE; PS00666; DHDPS_2; 1.
 KW Lyase; Diaminopimelate biosynthesis; Lysine biosynthesis;
 KW Complete proteome.
 FT ACT_SITE 162 162 BY SIMILARITY.
 SQ SEQUENCE 295 AA; 31643 MW; 56D3567076CD8FB5 CRC64;

Query Match 75.0%; Score 6; DB 1; Length 295;
 Best Local Similarity 100.0%; Pred. No. 9;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VNLDAE 7
 |||||
 Db 142 VNLDAE 147

RESULT 3

K1CR_XENLA
 ID K1CR_XENLA STANDARD; PRT; 368 AA.
 AC P08802;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Keratin, type I cytoskeletal endo B (Fragment).
 GN XK ENDO B.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipioidea; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89092007; PubMed=2463213;
 RA Laflamme S.E., Jamrich M., Richter K., Sargent T.D., Dawid I.B.;
 RT "Xenopus endo B is a keratin preferentially expressed in the
 RT embryonic notochord."
 RL Genes Dev. 2:853-862(1988).
 CC -!- SUBUNIT: Heterotetramer of two type I and two type II keratins.
 CC -!- MISCELLANEOUS: There are two types of cytoskeletal and
 CC microfibrillar keratin, I (acidic) and II (neutral to basic) (40-
 CC 55 and 56-70 kDa, respectively).
 CC -!- SIMILARITY: Belongs to the intermediate filament family.
 CC -----
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 CC -----
 DR EMBL; Y00230; CAA68372.1; -.
 DR PIR; A28825; A28825.
 DR InterPro; IPR001664; IF.
 DR InterPro; IPR002957; Keratin_I.
 DR Pfam; PF00038; filament; 1.

DR PRINTS; PR01248; TYPE1KERATIN.
 DR PROSITE; PS00226; IF; 1.
 KW Intermediate filament; Coiled coil; Keratin.
 FT NON_TER 1 1
 FT DOMAIN <1 15 HEAD.
 FT DOMAIN 16 325 ROD.
 FT DOMAIN 326 368 TAIL.
 FT DOMAIN 16 54 COIL 1A.
 FT DOMAIN 55 66 LINKER 1.
 FT DOMAIN 67 162 COIL 1B.
 FT DOMAIN 163 183 LINKER 12.
 FT DOMAIN 184 325 COIL 2.
 SQ SEQUENCE 368 AA; 41683 MW; 29FC19B67E9E8F95 CRC64;

Query Match 75.0%; Score 6; DB 1; Length 368;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VNLDAE 7
 |||||
 Db 220 VNLDAE 225

RESULT 4

ALR2_BACSU

ID ALR2_BACSU STANDARD; PRT; 394 AA.
 AC P94494;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Alanine racemase 2 (EC 5.1.1.1).
 GN ALR2 OR BSU17640.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Borchert S., Klein C., Piksa B., Hammelmann M., Entian K.D.;
 RT "Sequencing of a 26 kb region of the Bacillus subtilis genome
 downstream of spoVJ."
 RL Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=98044033; PubMed=9384377;
 RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
 Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
 Borriass R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
 Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
 Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
 Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
 Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
 Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
 Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
 Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
 Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
 Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,

RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
 RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
 RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
 RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
 RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
 RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
 RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
 RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
 RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
 RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
 RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
 RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
 RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
 RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
 RT "The complete genome sequence of the Gram-positive bacterium *Bacillus*
 RT *subtilis*.";
 RL Nature 390:249-256(1997).
 CC -!- FUNCTION: Provides the D-alanine required for cell wall
 CC biosynthesis (By similarity).
 CC -!- CATALYTIC ACTIVITY: L-alanine = D-alanine.
 CC -!- COFACTOR: Pyridoxal phosphate (By similarity).
 CC -!- PATHWAY: D-alanine branch of peptidoglycan biosynthesis; first
 CC step.
 CC -!- SIMILARITY: Belongs to the alanine racemase family.
 CC -----
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 CC -----
 DR EMBL; U66480; AAB41097.1; -.
 DR EMBL; Z99113; CAB13648.1; -.
 DR PIR; F69888; F69888.
 DR HSSP; P10724; 1BD0.
 DR SubtiList; BG12267; alr2.
 DR HAMAP; MF_01201; -; 1.
 DR InterPro; IPR000821; Ala_racemase.
 DR InterPro; IPR009006; Racem_decarbox_C.
 DR InterPro; IPR001608; UPF0001.
 DR Pfam; PF00842; Ala_racemase_C; 1.
 DR Pfam; PF01168; Ala_racemase_N; 1.
 DR PRINTS; PR00992; ALARACEMASE.
 DR TIGRFAMs; TIGR00492; alr; 1.
 DR PROSITE; PS00395; ALANINE_RACEMASE; 1.
 KW Isomerase; Pyridoxal phosphate; Cell wall; Peptidoglycan synthesis;
 KW Complete proteome.
 FT ACT_SITE 39 39 CATALYTIC BASE SPECIFIC TO D-ALANINE (BY
 FT SIMILARITY).
 FT ACT_SITE 272 272 CATALYTIC BASE SPECIFIC TO L-ALANINE (BY
 FT SIMILARITY).
 FT BINDING 39 39 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
 SQ SEQUENCE 394 AA; 43648 MW; FE446C21107FBA6E CRC64;

Query Match 75.0%; Score 6; DB 1; Length 394;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDA 6
 |||||
 Db 11 EVNLDA 16

RESULT 5

MBHL_ALCHY

ID MBHL_ALCHY STANDARD; PRT; 621 AA.
 AC P33374;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Uptake hydrogenase large subunit (EC 1.12.99.6) (Hydrogenlyase)
 DE (Membrane-bound hydrogenase large subunit).
 GN HUPL.
 OS Alcaligenes hydrogenophilus.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Alcaligenaceae; Alcaligenes.
 OX NCBI_TaxID=516;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93193199; PubMed=1294332;
 RA Yagi K., Seto T., Terakado M., Umeda F., Doi T., Imanishi T.,
 RA Miura Y.;
 RT "Nucleotide sequences of membrane-bound hydrogenase gene in
 RT Alcaligenes hydrogenophilus.";
 RL Chem. Pharm. Bull. 40:3292-3296(1992).
 CC -!- FUNCTION: This enzyme recycles the H(2) produced by nitrogenase to
 CC increase the production of ATP and to protect nitrogenase against
 CC inhibition or damage by O(2) under carbon- or phosphate-limited
 CC conditions.
 CC -!- CATALYTIC ACTIVITY: H(2) + acceptor = 2 H(+) + reduced acceptor.
 CC -!- COFACTOR: Binds 1 nickel ion per subunit (By similarity).
 CC -!- SUBUNIT: Heterodimer of a large and a small subunit.
 CC -!- SUBCELLULAR LOCATION: Membrane-bound.
 CC -!- SIMILARITY: Belongs to the [NiFe]/[NiFeSe] hydrogenase large
 CC subunit family.
 CC -----
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 CC -----
 DR EMBL; S56898; AAB25780.1; ALT_SEQ.
 DR PIR; JH0776; JH0776.
 DR HSSP; P21852; 1H2R.
 DR InterPro; IPR001501; Ni_hdL.
 DR Pfam; PF00374; NiFeSe_Hases; 1.
 DR PROSITE; PS00507; NI_HGENASE_L_1; FALSE_NEG.

DR PROSITE; PS00508; NI_HGENASE_L_2; 1.
 KW Oxidoreductase; Membrane; Metal-binding; Nickel.
 FT METAL 75 75 NICKEL (POTENTIAL).
 FT METAL 78 78 NICKEL (POTENTIAL).
 FT METAL 600 600 NICKEL (POTENTIAL).
 FT METAL 603 603 NICKEL (POTENTIAL).
 SQ SEQUENCE 621 AA; 68924 MW; 906AC4414285D4A3 CRC64;

Query Match 75.0%; Score 6; DB 1; Length 621;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVNLDA 6
 |||||
 Db 33 EVNLDA 38

RESULT 6

DYHC_DROME
 ID DYHC_DROME STANDARD; PRT; 4639 AA.
 AC P37276;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Dynein heavy chain, cytosolic (DYHC).
 GN CDHC OR DHC64C.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94375524; PubMed=8089180;
 RA Li M., McGrail M., Serr M., Hays T.S.;
 RT "Drosophila cytoplasmic dynein, a microtubule motor that is
 RT asymmetrically localized in the oocyte."
 RL J. Cell Biol. 126:1475-1494(1994).
 RN [2]
 RP SEQUENCE OF 1877-1998 FROM N.A.
 RX MEDLINE=94243034; PubMed=8186464;
 RA Rasmusson K., Serr M., Gepner J., Gibbons I., Hays T.S.;
 RT "A family of dynein genes in Drosophila melanogaster."
 RL Mol. Biol. Cell 5:45-55(1994).
 CC -!- FUNCTION: Cytoplasmic dynein acts as a motor for the intracellular
 CC retrograde motility of vesicles and organelles along microtubules.
 CC Dynein has ATPase activity; the force-producing power stroke is
 CC thought to occur on release of ADP.
 CC -!- SUBUNIT: Consists of at least two heavy chains and a number of
 CC intermediate and light chains.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- DOMAIN: Dynein heavy chains probably consist of an N-terminal stem
 CC (which binds cargo and interacts with other dynein components),
 CC and the head or motor domain. The motor contains six tandemly-
 CC linked AAA domains in the head, which form a ring. A stalk-like
 CC structure (formed by two of the coiled coil domains) protrudes
 CC between AAA 4 and AAA 5 and terminates in a microtubule-binding

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CC      site. A seventh domain may also contribute to this ring; it is not
CC      clear whether the N-terminus or the C-terminus forms this extra
CC      domain. There are four well-conserved and two non-conserved ATPase
CC      sites, one per AAA domain. Probably only one of these (within AAA
CC      1) actually hydrolyzes ATP, the others may serve a regulatory
CC      function.
CC      -!- SIMILARITY: Belongs to the dynein heavy chain family.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; L23195; AAA60323.1; -.
DR      EMBL; L25122; AAA28492.1; -.
DR      PIR; A54794; A54794.
DR      FlyBase; FBgn0010349; Dhc64C.
DR      GO; GO:0045169; C:fusome; NAS.
DR      GO; GO:0005875; C:microtubule associated complex; IDA.
DR      GO; GO:0008567; F:dynein ATPase activity; IDA.
DR      GO; GO:0003777; F:microtubule motor activity; IDA.
DR      GO; GO:0007098; P:centrosome cycle; IMP.
DR      GO; GO:0007292; P:female gamete generation; IMP.
DR      GO; GO:0045478; P:fusome organization and biogenesis; NAS.
DR      GO; GO:0007018; P:microtubule-based movement; IDA.
DR      GO; GO:0007294; P:oocyte cell fate determination (sensu Insecta); IMP.
DR      InterPro; IPR003593; AAA_ATPase.
DR      InterPro; IPR004273; Dynein_heavy.
DR      Pfam; PF03028; Dynein_heavy; 1.
DR      SMART; SM00382; AAA; 4.
KW      Motor protein; Dynein; Microtubule; ATP-binding; Repeat; Coiled coil.
FT      DOMAIN      1      1856      STEM (BY SIMILARITY).
FT      DOMAIN      1857      2084      AAA 1 (BY SIMILARITY).
FT      DOMAIN      2166      2437      AAA 2 (BY SIMILARITY).
FT      DOMAIN      2541      2790      AAA 3 (BY SIMILARITY).
FT      DOMAIN      2884      3153      AAA 4 (BY SIMILARITY).
FT      DOMAIN      3189      3478      STALK (BY SIMILARITY).
FT      DOMAIN      3539      3768      AAA 5 (BY SIMILARITY).
FT      DOMAIN      3989      4205      AAA 6 (BY SIMILARITY).
FT      DOMAIN      530      565      COILED COIL (POTENTIAL).
FT      DOMAIN      774      794      COILED COIL (POTENTIAL).
FT      DOMAIN      1264      1368      COILED COIL (POTENTIAL).
FT      DOMAIN      3189      3261      COILED COIL (POTENTIAL).
FT      DOMAIN      3382      3478      COILED COIL (POTENTIAL).
FT      DOMAIN      3723      3782      COILED COIL (POTENTIAL).
FT      NP_BIND      1895      1902      ATP (POTENTIAL).
FT      NP_BIND      2210      2217      ATP (POTENTIAL).
FT      NP_BIND      2580      2587      ATP (POTENTIAL).
FT      NP_BIND      2922      2929      ATP (POTENTIAL).
SQ      SEQUENCE      4639 AA; 530152 MW; 057A7D8800CCD07E CRC64;

Query Match      75.0%; Score 6; DB 1; Length 4639;
Best Local Similarity 100.0%; Pred. No. 85;
Matches      6; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

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Qy 3 NLDAEF 8
 | | | | |
Db 3885 NLDAEF 3890

RESULT 7

RGS3_RAT

ID RGS3_RAT STANDARD; PRT; 67 AA.
AC P49797;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Regulator of G-protein signaling 3 (RGS3) (Fragment).
GN RGS3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=96140645; PubMed=8548815;
RA Koelle M.R., Horvitz H.R.;
RT "EGL-10 regulates G protein signaling in the C. elegans nervous
RT system and shares a conserved domain with many mammalian proteins.";
RL Cell 84:115-125(1996).
RN [2]
RP PHOSPHORYLATION.
RX MEDLINE=20167219; PubMed=10702309;
RA Pedram A., Razandi M., Kehrl J., Levin E.R.;
RT "Natriuretic peptides inhibit G protein activation. Mediation through
RT cross-talk between cyclic GMP-dependent protein kinase and regulators
RT of G protein-signaling proteins.";
RL J. Biol. Chem. 275:7365-7372(2000).
CC -!- FUNCTION: Inhibits signal transduction by increasing the GTPase
CC activity of G protein alpha subunits thereby driving them into
CC their inactive GDP-bound form.
CC -!- PTM: Phosphorylated by cyclic GMP-dependent protein kinase.
CC -!- SIMILARITY: Contains 1 RGS domain.
CC -----
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CC -----
DR EMBL; U32434; AAC52371.1; -.
DR HSSP; P49799; 1AGR.
DR InterPro; IPR000342; Regl_Gprotein.
DR Pfam; PF00615; RGS; 1.
DR PRINTS; PR01301; RGSPROTEIN.
DR PROSITE; PS50132; RGS; 1.
KW Signal transduction inhibitor; Phosphorylation.
FT NON_TER 1 1

FT DOMAIN <1 >67 RGS.
 FT NON_TER 67 67
 SQ SEQUENCE 67 AA; 7641 MW; 06FE7630E1CE3AF5 CRC64;

Query Match 62.5%; Score 5; DB 1; Length 67;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVNLD 5
 |||||
 Db 34 EVNLD 38

RESULT 8

PHD_BPP1

ID PHD_BPP1 STANDARD; PRT; 73 AA.
 AC Q06253;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Prevent host death protein.
 GN PHD.
 OS Bacteriophage P1.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
 OC P1-like viruses.
 OX NCBI_TaxID=10678;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94016561; PubMed=8411153;
 RA Lehnherr H., Maguin E., Jafri S., Yarmolinsky M.B.;
 RT "Plasmid addiction genes of bacteriophage P1: doc, which causes cell
 RT death on curing of prophage, and phd, which prevents host death when
 RT prophage is retained."
 RL J. Mol. Biol. 233:414-428(1993).
 CC -!- FUNCTION: Antidote to the toxic effect of the doc protein on
 CC the host. Phd and doc proteins function in unisson to stabilize
 CC plasmid number by inducing a lethal response to plasmid loss.
 CC -!- MISCELLANEOUS: The concentration of phd in P1 lysogens is far
 CC greater than that of the poison it antagonizes. Such an excess may
 CC assume the well-being of carriers of the addicting plasmid.
 CC -!- SIMILARITY: BELONGS TO THE PHD/YEFM FAMILY.
 CC -----
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 CC -----
 DR EMBL; M95666; AAA16932.1; -.
 DR PIR; S40015; S40015.
 DR InterPro; IPR006442; Phd_fam.
 DR TIGRFAMs; TIGR01552; phd_fam; 1.
 FT DOMAIN 57 73 NON-ESSENTIAL FOR ACTIVITY.
 SQ SEQUENCE 73 AA; 8133 MW; 5FDB9D3565440050 CRC64;

Query Match 62.5%; Score 5; DB 1; Length 73;
 Best Local Similarity 100.0%; Pred. No. 34;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LDAEF 8
 |||||
 Db 52 LDAEF 56

RESULT 9

EF1B_SULSO

ID EF1B_SULSO STANDARD; PRT; 90 AA.
 AC Q64214;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Elongation factor 1-beta (EF-1-beta) (aEF-1beta).
 GN EF1B OR SSO5345.
 OS Sulfolobus solfataricus.
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
 OC Sulfolobus.
 OX NCBI_TaxID=2287;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-11 AND 82-90.
 RC STRAIN=ATCC 49255 / DSM 5833 / MT-4;
 RX MEDLINE=95359209; PubMed=7632739;
 RA Arcari P., Raimo G., Ianniciello G., Gallo M., Bocchini V.;
 RT "The first nucleotide sequence of an archaeal elongation factor 1
 RT beta gene.";
 RL Biochim. Biophys. Acta 1263:86-88(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 35092 / DSM 1617 / P2;
 RX MEDLINE=21332296; PubMed=11427726;
 RA She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
 RA Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
 RA De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,
 RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
 RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
 RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
 RA Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;
 RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
 RN [3]
 RP SEQUENCE, FUNCTION, SUBUNITS, AND MASS SPECTROMETRY.
 RC STRAIN=ATCC 49255 / DSM 5833 / MT-4;
 RX MEDLINE=96186282; PubMed=8652615;
 RA Raimo G., Masullo M., Savino G., Scarano G., Ianniciello G.,
 RA Parente A., Bocchini V.;
 RT "Archaeal elongation factor 1 beta is a dimer. Primary structure,
 RT molecular and biochemical properties.";
 RL Biochim. Biophys. Acta 1293:106-112(1996).
 CC -!- FUNCTION: Promotes the exchange of GDP for GTP in EF-1-alpha/GDP,
 CC thus allowing the regeneration of EF-1-alpha/GTP that could then
 CC be used to form the ternary complex EF-1-alpha/GTP/AArRNA.
 CC -!- SUBUNIT: Homodimer.
 CC -!- MASS SPECTROMETRY: MW=10006; METHOD=Electrospray.

CC -!- SIMILARITY: Belongs to the EF-1-beta/EF-1-delta family.
 CC -----
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 CC -----
 DR EMBL; X76768; CAA54164.1; -.
 DR EMBL; AE006655; AAK40523.1; -.
 DR PIR; S57268; S57268.
 DR HSSP; O27734; 1GH8.
 DR HAMAP; MF_00043; -, 1.
 DR InterPro; IPR004542; aEF-1_beta.
 DR InterPro; IPR001326; EF1_BD.
 DR Pfam; PF00736; EF1BD; 1.
 DR TIGRFAMs; TIGR00489; aEF-1_beta; 1.
 KW Elongation factor; Protein biosynthesis; Complete proteome.
 FT INIT_MET 0 0
 SQ SEQUENCE 90 AA; 10005 MW; 24CB357FD3259C8A CRC64;

Query Match 62.5%; Score 5; DB 1; Length 90;
 Best Local Similarity 100.0%; Pred. No. 41;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVNLD 5
 |||||
 Db 15 EVNLD 19

RESULT 10

EF1B_PYRAB

ID EF1B_PYRAB STANDARD; PRT; 91 AA.
 AC Q9V2P6;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Elongation factor 1-beta (EF-1-beta) (aEF-1beta).
 GN EF1B OR PYRAB00290 OR PAB3009.
 OS Pyrococcus abyssi.
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 OC Pyrococcus.
 OX NCBI_TaxID=29292;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GE5 / Orsay;
 RX MEDLINE=22511545; PubMed=12622808;
 RA Cohen G.N., Barbe V., Flament D., Galperin M., Heilig R., Lecompte O.,
 RA Poch O., Prieur D., Querellou J., Ripp R., Thierry J.-C.,
 RA Van der Oost J., Weissenbach J., Zivanovic Y., Forterre P.;
 RT "An integrated analysis of the genome of the hyperthermophilic
 RT archaeon Pyrococcus abyssi."
 RL Mol. Microbiol. 47:1495-1512(2003).
 CC -!- FUNCTION: Promotes the exchange of GDP for GTP in EF-1-alpha/GDP,
 CC thus allowing the regeneration of EF-1-alpha/GTP that could then

CC be used to form the ternary complex EF-1-alpha/GTP/AAtRNA (By
CC similarity).
CC -!- SIMILARITY: Belongs to the EF-1-beta/EF-1-delta family.

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CC -----

DR EMBL; AJ248283; CAB48952.1; -.
DR PIR; A75188; A75188.
DR HSSP; O27734; 1GH8.
DR HAMAP; MF_00043; -; 1.
DR InterPro; IPR004542; aEF-1_beta.
DR InterPro; IPR001326; EF1_BD.
DR Pfam; PF00736; EF1BD; 1.
DR TIGRFAMs; TIGR00489; aEF-1_beta; 1.
KW Elongation factor; Protein biosynthesis; Complete proteome.
SQ SEQUENCE 91 AA; 10239 MW; 45A032D81D54F1EA CRC64;

Query Match 62.5%; Score 5; DB 1; Length 91;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLD 5
| | | | |
Db 18 EVNLD 22

RESULT 11

EF1B_PYRFU

ID EF1B_PYRFU STANDARD; PRT; 91 AA.
AC Q8TZM5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Elongation factor 1-beta (EF-1-beta) (aEF-1beta).
GN EF1B OR PF1965.
OS Pyrococcus furiosus.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=2261;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Vc1 / DSM 3638 / ATCC 43587 / JCM 8422;
RA Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
RT "The complete sequence of the Pyrococcus furiosus genome."
RL Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
CC -!- FUNCTION: Promotes the exchange of GDP for GTP in EF-1-alpha/GDP,
CC thus allowing the regeneration of EF-1-alpha/GTP that could then
CC be used to form the ternary complex EF-1-alpha/GTP/AAtRNA (By
CC similarity).
CC -!- SIMILARITY: Belongs to the EF-1-beta/EF-1-delta family.
CC -----

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CC -----

DR EMBL; AE010290; AAL82089.1; -.
DR HAMAP; MF_00043; -; 1.
DR InterPro; IPR004542; aEF-1_beta.
DR InterPro; IPR001326; EF1_BD.
DR Pfam; PF00736; EF1BD; 1.
DR TIGRFAMs; TIGR00489; aEF-1_beta; 1.
KW Elongation factor; Protein biosynthesis; Complete proteome.
SQ SEQUENCE 91 AA; 10322 MW; C54B247AEC77136C CRC64;

Query Match 62.5%; Score 5; DB 1; Length 91;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLD 5
| | | | |
Db 18 EVNLD 22

RESULT 12

EF1B_SULTO

ID EF1B_SULTO STANDARD; PRT; 91 AA.
AC Q976H8;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Elongation factor 1-beta (EF-1-beta) (aEF-1beta).
GN EF1B OR ST0208.2 OR STS027.
OS Sulfolobus tokodaii.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=111955;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JCM 10545 / 7;
RX MEDLINE=21456156; PubMed=11572479;
RA Kawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
RA Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,
RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
RA Oshima T., Kikuchi H.;
RT "Complete genome sequence of an aerobic thermoacidophilic
RT Crenarchaeon, Sulfolobus tokodaii strain7.";
RL DNA Res. 8:123-140(2001).
CC -!- FUNCTION: Promotes the exchange of GDP for GTP in EF-1-alpha/GDP,
CC thus allowing the regeneration of EF-1-alpha/GTP that could then
CC be used to form the ternary complex EF-1-alpha/GTP/AA-tRNA (By
CC similarity).
CC -!- SIMILARITY: Belongs to the EF-1-beta/EF-1-delta family.

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CC -----
DR EMBL; AP000981; BAB65169.1; -.
DR HAMAP; MF_00043; -, 1.
DR InterPro; IPR004542; aEF-1_beta.
DR InterPro; IPR001326; EF1_BD.
DR Pfam; PF00736; EF1BD; 1.
DR TIGRFAMs; TIGR00489; aEF-1_beta; 1.
KW Elongation factor; Protein biosynthesis; Complete proteome.
SQ SEQUENCE 91 AA; 10006 MW; E8649D4646DC348B CRC64;

```

```

Query Match          62.5%; Score 5; DB 1; Length 91;
Best Local Similarity 100.0%; Pred. No. 41;
Matches      5; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 EVNLD 5
        |||||
Db      16 EVNLD 20

```

RESULT 13

KM11_TRYBB

```

ID KM11_TRYBB STANDARD; PRT; 92 AA.
AC Q26773;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Kinetoplastid membrane protein-11 (KMP-11).
GN KMP-11/1 AND KMP-11/2 AND KMP-11/3 AND KMP-11/4.
OS Trypanosoma brucei brucei, and
OS Trypanosoma brucei rhodesiense.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5702, 31286;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 32-45.
RC SPECIES=T.b.rhodesiense; STRAIN=ViTat 1.1;
RX MEDLINE=97047387; PubMed=8892307;
RA Stebeck C.E., Baron G.S., Beecroft R.P., Pearson T.W.;
RT "Molecular characterization of the kinetoplastid membrane protein-11
RT from African trypanosomes.";
RL Mol. Biochem. Parasitol. 81:81-88(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=T.b.brucei;
RX MEDLINE=98226179; PubMed=9566527;
RA Bridge M.A., Zhou Q., Koop B.F., Pearson T.W.;
RT "Cloning and characterization of the kinetoplastid membrane protein-11
RT gene locus of Trypanosoma brucei.";
RL Mol. Biochem. Parasitol. 91:359-363(1998).
RN [3]

```

RP SUBCELLULAR LOCATION.
RX MEDLINE=95356787; PubMed=7630374;
RA Stebeck C.E., Beecroft R.P., Singh B.N., Jardim A., Olafson R.W.,
RA Tuckey C., Prenevost K.D., Pearson T.W.;
RT "Kinetoplastid membrane protein-11 (KMP-11) is differentially
RT expressed during the life cycle of African trypanosomes and is found
RT in a wide variety of kinetoplastid parasites.";
RL Mol. Biochem. Parasitol. 71:1-13(1995).
CC -!- FUNCTION: May be involved in the regulation of the cytoskeleton
CC through interaction with the subpellicular microtubules. May be
CC involved in parasite mobility and attachment to the surface of the
CC host cell. Behaves as a strong immunogen during infection (By
CC similarity).
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic. Associated with microtubules.
CC -!- MISCELLANEOUS: There are four copies of the KMP-11 gene in
CC T.b.brucei while a single copy of the gene is found in
CC T.b.rhodesiense.
CC -!- SIMILARITY: Belongs to the KMP-11 family.
CC -----
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CC -----
DR EMBL; X96439; CAA65305.1; -.
DR EMBL; AF028726; AAC38990.1; -.
DR EMBL; AF028726; AAC38991.1; -.
DR EMBL; AF028726; AAC38992.1; -.
DR EMBL; AF028726; AAC38993.1; -.
DR GO; GO:0015630; C:microtubule cytoskeleton; ISS.
DR GO; GO:0030260; P:cell invasion; ISS.
DR GO; GO:0001539; P:ciliary/flagellar motility; ISS.
DR GO; GO:0007010; P:cytoskeleton organization and biogenesis; ISS.
DR InterPro; IPR004132; KMP11.
DR Pfam; PF03037; KMP11; 1.
KW Antigen; Cytoskeleton; Microtubule; Multigene family.
SQ SEQUENCE 92 AA; 11076 MW; B50328C81A770E4C CRC64;

Query Match 62.5%; Score 5; DB 1; Length 92;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LDAEF 8
| | | | |
Db 15 LDAEF 19

RESULT 14

KM11_TRYCR

ID KM11_TRYCR STANDARD; PRT; 92 AA.
AC Q9U6Z1; O21435; Q9U6Z0;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Kinetoplastid membrane protein-11 (KMP-11).
 GN KMP-11 OR KMP11.
 OS Trypanosoma cruzi.
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
 OX NCBI_TaxID=5693;
 RN [1]
 RP SEQUENCE FROM N.A., SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.
 RC STRAIN=Tulahuen, and Y;
 RX MEDLINE=20132225; PubMed=10668791;
 RA Thomas M.C., Garcia-Perez J.L., Alonso C., Lopez M.C.;
 RT "Molecular characterization of KMP11 from Trypanosoma cruzi: a
 RT cytoskeleton-associated protein regulated at the translational
 RT level.";
 RL DNA Cell Biol. 19:47-57(2000).
 RN [2]
 RP FUNCTION.
 RX MEDLINE=21195155; PubMed=11298135;
 RA Thomas M.C., Longobardo M.V., Carmelo E., Maranon C., Planelles L.,
 RA Patarroyo M.E., Alonso C., Lopez M.C.;
 RT "Mapping of the antigenic determinants of the T. cruzi kinetoplastid
 RT membrane protein-11. Identification of a linear epitope specifically
 RT recognized by human Chagasic sera.";
 RL Clin. Exp. Immunol. 123:465-471(2001).
 CC -!- FUNCTION: May be involved in the regulation of the cytoskeleton
 CC through interaction with the subpellicular microtubules. May be
 CC involved in parasite mobility and attachment to the surface of the
 CC host cell. Behaves as a strong immunogen during infection.
 CC -!- SUBUNIT: Monomer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic. Associated with microtubules.
 CC -!- DEVELOPMENTAL STAGE: Abundantly expressed in amastigotes and
 CC trypomastigotes. In epimastigotes, KMP-11 is expressed at a high
 CC level during the logarithmic growth phase but is downregulated
 CC during the stationary phase of growth.
 CC -!- MISCELLANEOUS: There are four copies of the KMP-11 gene in
 CC T.cruzi.
 CC -!- SIMILARITY: Belongs to the KMP-11 family.
 CC -----
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 CC -----
 DR EMBL; AJ000077; CAA03901.1; -.
 DR EMBL; AF167435; AAF04809.1; -.
 DR EMBL; AF167436; AAF04810.1; -.
 DR GO; GO:0015630; C:microtubule cytoskeleton; IDA.
 DR GO; GO:0030260; P:cell invasion; NAS.
 DR GO; GO:0001539; P:ciliary/flagellar motility; NAS.
 DR GO; GO:0007010; P:cytoskeleton organization and biogenesis; IDA.
 DR InterPro; IPR004132; KMP11.
 DR Pfam; PF03037; KMP11; 1.
 KW Antigen; Cytoskeleton; Microtubule; Multigene family.
 FT CONFLICT 92 92 MISSING (IN REF. 1; AAF04809).

SQ SEQUENCE 92 AA; 11011 MW; 341CDD0E21D3EFB1 CRC64;

Query Match 62.5%; Score 5; DB 1; Length 92;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LDAEF 8
|||||
Db 15 LDAEF 19

RESULT 15

ACPS_BACHD

ID ACPS_BACHD STANDARD; PRT; 119 AA.

AC Q9KFG1;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Holo-[acyl-carrier protein] synthase (EC 2.7.8.7) (Holo-ACP synthase)

DE (4'-phosphopantetheinyl transferase acps).

GN ACPS OR BH0518.

OS Bacillus halodurans.

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

OX NCBI_TaxID=86665;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C-125 / JCM 9153;

RX MEDLINE=20512582; PubMed=11058132;

RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,

RA Fuji F., Hiramata C., Nakamura Y., Ogasawara N., Kuhara S.,

RA Horikoshi K.;

RT "Complete genome sequence of the alkaliphilic bacterium Bacillus

RT halodurans and genomic sequence comparison with Bacillus subtilis.";

RL Nucleic Acids Res. 28:4317-4331(2000).

CC -!- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme
CC A to a Ser of acyl-carrier protein (By similarity).

CC -!- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine
CC 3',5'-bisphosphate + holo-[acyl-carrier protein].

CC -!- COFACTOR: Magnesium (By similarity).

CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

CC -!- SIMILARITY: Belongs to the P-Pant transferase superfamily. AcpS
CC family.

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CC -----
DR EMBL; AP001508; BAB04237.1; -.

DR PIR; F83714; F83714.

DR HAMAP; MF_00101; -; 1.

DR InterPro; IPR008278; 4-PPT_transf.

DR InterPro; IPR002582; ACPS.

DR InterPro; IPR004568; Pantethn_trn.

DR Pfam; PF01648; ACPS; 1.
 DR ProDom; PD004282; ACPS; 1.
 DR TIGRFAMs; TIGR00516; acps; 1.
 DR TIGRFAMs; TIGR00556; pantethn_trn; 1.
 KW Transferase; Lipid synthesis; Fatty acid biosynthesis; Magnesium;
 KW Complete proteome.
 FT METAL 8 8 MAGNESIUM (BY SIMILARITY).
 FT METAL 58 58 MAGNESIUM (BY SIMILARITY).
 SQ SEQUENCE 119 AA; 13421 MW; 2279E552549041C9 CRC64;

Query Match 62.5%; Score 5; DB 1; Length 119;
 Best Local Similarity 100.0%; Pred. No. 51;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VNLDA 6
 |||||
 Db 91 VNLDA 95

RESULT 16

PFD4 CAEEL

ID PFD4 CAEEL STANDARD; PRT; 126 AA.
 AC Q17435;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Probable prefoldin subunit 4.
 GN B0035.4.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA White S.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Kohara Y., Shin'i T., Suzuki Y., Sugano S., Potdevin M.,
 RA Thierry-Mieg Y., Thierry-Mieg D., Thierry-Mieg J.;
 RL Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
 CC -!- FUNCTION: Binds specifically to cytosolic chaperonin (c-CPN) and
 CC transfers target proteins to it. Binds to nascent polypeptide
 CC chain and promotes folding in an environment in which there are
 CC many competing pathways for nonnative proteins (By similarity).
 CC -!- SUBUNIT: Heterohexamer of two PFD-alpha type and four PFD-beta
 CC type subunits (By similarity).
 CC -!- SIMILARITY: Belongs to the prefoldin beta subunit family.

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CC

DR EMBL; Z73102; CAA97410.1; -.

DR EMBL; AF292051; AAG41147.1; -.

DR PIR; T18655; T18655.

DR WormPep; B0035.4; CE05162.

KW Chaperone.

SQ SEQUENCE 126 AA; 14031 MW; 22D8B5B370AB4DE8 CRC64;

Query Match 62.5%; Score 5; DB 1; Length 126;

Best Local Similarity 100.0%; Pred. No. 53;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 NLDAE 7

||||

Db 121 NLDAE 125

RESULT 17

GREA_CHLTE

ID GREA_CHLTE STANDARD; PRT; 159 AA.

AC Q8KCH5;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Transcription elongation factor greA (Transcript cleavage factor greA).

GN GREA OR CT1446.

OS Chlorobium tepidum.

OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;

OC Chlorobium.

OX NCBI_TaxID=1097;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=TLS / ATCC 49652 / DSM 12025;

RX MEDLINE=22103685; PubMed=12093901;

RA Eisen J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M.,

RA Dodson R.J., Deboy R., Gwinn M.L., Nelson W.C., Haft D.H.,

RA Hickey E.K., Peterson J.D., Durkin A.S., Kolonay J.L., Yang F.,

RA Holt I., Umayam L.A., Mason T., Brenner M., Shea T.P., Parksey D.,

RA Nierman W.C., Feldblyum T.V., Hansen C.L., Craven M.B., Radune D.,

RA Vamathevan J., Khouri H., White O., Gruber T.M., Ketchum K.A.,

RA Venter J.C., Tettelin H., Bryant D.A., Fraser C.M.;

RT "The complete genome sequence of Chlorobium tepidum TLS, a

RT photosynthetic, anaerobic, green-sulfur bacterium.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514(2002).

CC -!- FUNCTION: Necessary for efficient RNA polymerase transcription
CC elongation past template-encoded arresting sites. The arresting
CC sites in DNA have the property of trapping a certain fraction of
CC elongating RNA polymerases that pass through, resulting in locked
CC ternary complexes. Cleavage of the nascent transcript by cleavage
CC factors such as greA or greB allows the resumption of elongation
CC from the new 3'terminus. GreA releases sequences of 2 to 3
CC nucleotides (By similarity).

CC -!- SIMILARITY: Belongs to the greA/greB family.

CC

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CC -----

DR EMBL; AE012902; AAM72674.1; -.
DR TIGR; CT1446; -.
DR HAMAP; MF_00105; -; 1.
DR InterPro; IPR006359; GreA.
DR InterPro; IPR001437; GreA_GreB.
DR Pfam; PF01272; GreA_GreB; 1.
DR Pfam; PF03449; GreA_GreB_N; 1.
DR ProDom; PD004918; GreA_GreB; 1.
DR TIGRFAMs; TIGR01462; greA; 1.
DR PROSITE; PS00829; GREAB_1; 1.
DR PROSITE; PS00830; GREAB_2; 1.
KW Transcription regulation; DNA-binding; Coiled coil; Complete proteome.
FT DOMAIN 43 76 COILED COIL (POTENTIAL).
SQ SEQUENCE 159 AA; 17949 MW; 2B59B2DAE2409AB0 CRC64;

Query Match 62.5%; Score 5; DB 1; Length 159;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NLDAE 7
| | | | |
Db 96 NLDAE 100

RESULT 18

YFIR_ECOLI

ID YFIR_ECOLI STANDARD; PRT; 172 AA.
AC P76597;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein yfiR precursor.
GN YFIR OR B2603 OR Z3897 OR ECS3466.
OS Escherichia coli, and
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562, 83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12."
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.

RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
 RX MEDLINE=21074935; PubMed=11206551;
 RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
 RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
 RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
 RA Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
 RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
 RA Welch R.A., Blattner F.R.;
 RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7";
 RL Nature 409:529-533(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=O157:H7 / RIMD 0509952;
 RX MEDLINE=21156231; PubMed=11258796;
 RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
 RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
 RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
 RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
 RT "Complete genome sequence of enterohemorrhagic Escherichia coli
 RT O157:H7 and genomic comparison with a laboratory strain K-12";
 RL DNA Res. 8:11-22(2001).

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DR EMBL; AE000346; AAC75652.1; -.
 DR EMBL; AE005490; AAG57714.1; -.
 DR EMBL; AP002562; BAB36889.1; -.
 DR PIR; B91062; B91062.
 DR PIR; F65038; F65038.
 DR PIR; F85906; F85906.
 DR EcoGene; EGI4225; yfiR.
 KW Hypothetical protein; Signal; Complete proteome.
 FT SIGNAL 1 22 POTENTIAL.
 FT CHAIN 23 172 HYPOTHETICAL PROTEIN YFIR.
 SQ SEQUENCE 172 AA; 18978 MW; 2E2CC812E49F3AD5 CRC64;

Query Match 62.5%; Score 5; DB 1; Length 172;
 Best Local Similarity 100.0%; Pred. No. 69;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VNLDA 6
 |||||
 Db 146 VNLDA 150

RESULT 19
 KAD1_ANASP
 ID KAD1_ANASP STANDARD; PRT; 184 AA.
 AC Q8YPJ8;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Adenylate kinase 1 (EC 2.7.4.3) (ATP-AMP transphosphorylase 1).
 GN ADK1 OR ALL4196.
 OS Anabaena sp. (strain PCC 7120).
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
 OX NCBI_TaxID=103690;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21595285; PubMed=11759840;
 RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
 RA Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
 RA Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,
 RA Yasuda M., Tabata S.;
 RT "Complete genomic sequence of the filamentous nitrogen-fixing
 RT cyanobacterium Anabaena sp. strain PCC 7120."
 RL DNA Res. 8:205-213(2001).
 CC -!- FUNCTION: This small ubiquitous enzyme is essential for
 CC maintenance and cell growth.
 CC -!- CATALYTIC ACTIVITY: ATP + AMP = ADP + ADP.
 CC -!- SUBUNIT: Monomer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -!- SIMILARITY: Belongs to the adenylate kinase family.
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 CC -----
 DR EMBL; AP003595; BAB75895.1; -.
 DR PIR; AE2330; AE2330.
 DR HAMAP; MF_00235; -; 1.
 DR InterPro; IPR006259; Adenyl_kin_sub.
 DR InterPro; IPR000850; Adenylate_kin.
 DR Pfam; PF00406; ADK; 1.
 DR PRINTS; PR00094; ADENYLTKNASE.
 DR ProDom; PD000657; Adenylate_kin; 1.
 DR TIGRFAMs; TIGR01351; adk; 1.
 DR PROSITE; PS00113; ADENYLATE_KINASE; 1.
 KW Transferase; Kinase; ATP-binding; Complete proteome.
 FT NP_BIND 8 16 ATP (BY SIMILARITY).
 SQ SEQUENCE 184 AA; 20442 MW; A0CEDB1170D93B69 CRC64;

Query Match 62.5%; Score 5; DB 1; Length 184;
 Best Local Similarity 100.0%; Pred. No. 73;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VNLDA 6
 |||||
 Db 112 VNLDA 116

RESULT 20
 TBP_METKA

ID TBP_METKA STANDARD; PRT; 185 AA.
AC Q8TX38;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE TATA-box binding protein (TATA-box factor) (TATA sequence-binding
DE protein) (TBP) (Box A binding protein) (BAP).
GN TBP OR MK0839.
OS Methanopyrus kandleri.
OC Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
OC Methanopyrus.
OX NCBI_TaxID=2320;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AV19 / DSM 6324 / JCM 9639;
RX MEDLINE=21927647; PubMed=11930014;
RA Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N.,
RA Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,
RA Natale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,
RA Malykh A.G., Koonin E.V., Kozyavkin S.A.;
RT "The complete genome of hyperthermophile Methanopyrus kandleri AV19
RT and monophyly of archaeal methanogens.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).
CC -!- FUNCTION: General factor that plays a role in the activation of
CC archaeal genes transcribed by RNA polymerase. Binds specifically
CC to the TATA box promoter element which lies close to the position
CC of transcription initiation (By similarity).
CC -!- SIMILARITY: Belongs to the TBP family.
CC -----
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CC -----
DR EMBL; AE010374; AAM02052.1; -.
DR HAMAP; MF_00408; -; 1.
DR InterPro; IPR000814; TFIID.
DR Pfam; PF00352; TBP; 2.
DR PRINTS; PR00686; TIFACTORIID.
DR PROSITE; PS00351; TFIID; FALSE_NEG.
KW Transcription regulation; DNA-binding; Repeat; Complete proteome.
FT REPEAT 3 78 1.
FT REPEAT 94 176 2.
SQ SEQUENCE 185 AA; 20730 MW; 986CDA328B72E1B3 CRC64;

Query Match 62.5%; Score 5; DB 1; Length 185;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLD 5
| | | | |
Db 15 EVNLD 19

RESULT 21

OM26_HAEIN

ID OM26_HAEIN STANDARD; PRT; 197 AA.
AC Q57483; Q9S690; Q9S691; Q9S692; Q9S699;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Outer membrane protein 26 precursor.
GN OMP26 OR SKP OR HI0916.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
RT Rd.";
RL Science 269:496-512(1995).
RN [2]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN=NTHI 289, UC1, UC2, and UC10;
RX MEDLINE=99185023; PubMed=10085039;
RA El-Adhami W., Kyd J.M., Bastin D.A., Cripps A.W.;
RT "Characterization of the gene encoding a 26-kilodalton protein (OMP26)
RT from nontypeable Haemophilus influenzae and immune responses to the
RT recombinant protein.";
RL Infect. Immun. 67:1935-1942(1999).
RN [3]
RP SEQUENCE OF 24-30.
RX MEDLINE=20137488; PubMed=10675023;
RA Langen H., Takacs B., Evers S., Berndt P., Lahm H.W., Wipf B.,
RA Gray C., Fountoulakis M.;
RT "Two-dimensional map of the proteome of Haemophilus influenzae.";
RL Electrophoresis 21:411-429(2000).
CC -!- SUBCELLULAR LOCATION: Outer membrane.
CC -!- SIMILARITY: BELONGS TO THE OMPH/HLPA FAMILY.
CC -----
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CC -----
DR EMBL; U32773; AAC22574.1; -.

DR EMBL; AF109085; AAD23967.1; -.
 DR EMBL; AF109086; AAD23968.1; -.
 DR EMBL; AF109087; AAD23969.1; -.
 DR EMBL; AF109094; AAD23976.1; -.
 DR PIR; E64102; E64102.
 DR TIGR; HI0916; -.
 DR InterPro; IPR005632; OmpH.
 DR Pfam; PF03938; OmpH; 1.
 KW Outer membrane; Signal; Complete proteome.
 FT SIGNAL 1 23
 FT CHAIN 24 197 OUTER MEMBRANE PROTEIN 26.
 FT VARIANT 102 102 Q -> E (IN STRAINS NTHI 289 AND UC1).
 FT VARIANT 146 146 D -> N (IN STRAIN UC1).
 FT VARIANT 157 157 K -> R (IN STRAINS NTHI 289 AND UC10).
 FT VARIANT 170 170 I -> V (IN STRAINS NTHI 289, UC1 AND UC2).
 SQ SEQUENCE 197 AA; 21718 MW; 0C53927521EDB5DC CRC64;

Query Match 62.5%; Score 5; DB 1; Length 197;
 Best Local Similarity 100.0%; Pred. No. 77;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LDAEF 8
 |||||
 Db 49 LDAEF 53

RESULT 22

YDB6_YEAST

ID YDB6_YEAST STANDARD; PRT; 197 AA.
 AC Q12055;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical 22.7 kDa protein in CDC36-NRP1 intergenic region.
 GN YDL166C.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288c;
 RA Pohl T.M.;
 RL Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
 CC -!- SIMILARITY: Belongs to the UPF0101 family.

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 CC -----

DR EMBL; Z67750; CAA91580.1; -.
 DR EMBL; Z74214; CAA98740.1; -.

DR PIR; S61047; S61047.
 DR GermOnline; 140409; -.
 DR SGD; S0002325; YDL166C.
 DR GO; GO:0005634; C:nucleus; IDA.
 DR GO; GO:0006979; P:response to oxidative stress; IMP.
 KW Hypothetical protein; ATP-binding.
 FT NP_BIND 14 21 ATP (POTENTIAL).
 SQ SEQUENCE 197 AA; 22723 MW; 836A25B0D7E2633C CRC64;

Query Match 62.5%; Score 5; DB 1; Length 197;
 Best Local Similarity 100.0%; Pred. No. 77;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NLDAE 7
 |||||
 Db 124 NLDAE 128

RESULT 23

GDIR_YEAST

ID GDIR_YEAST STANDARD; PRT; 202 AA.
 AC Q12434;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Rho GDP-dissociation inhibitor (Rho GDI).
 GN RDI1 OR YDL135C OR D2175.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94327511; PubMed=8051050;
 RA Masuda T., Tanaka K., Nonaka H., Yamochi W., Maeda A., Takai Y.;
 RT "Molecular cloning and characterization of yeast rho GDP dissociation
 RT inhibitor.";
 RL J. Biol. Chem. 269:19713-19718(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288c / FY1679;
 RX MEDLINE=97127826; PubMed=8972577;
 RA Woelfl S., Haneman V., Saluz H.P.;
 RT "Analysis of a 26,756 bp segment from the left arm of yeast
 RT chromosome IV.";
 RL Yeast 12:1549-1554(1996).
 CC -!- FUNCTION: Regulates the GDP/GTP exchange reaction of the Rho
 CC proteins by inhibiting the dissociation of GDP from them, and the
 CC subsequent binding of GTP to them.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: Belongs to the Rho GDI family.
 CC -----
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CC -----

DR EMBL; D31630; BAA06499.1; -.
DR EMBL; X96876; CAA65624.1; -.
DR EMBL; Z74183; CAA98708.1; -.
DR PIR; A53646; A53646.
DR HSSP; P52566; 1DS6.
DR GermOnline; 140378; -.
DR SGD; S0002294; RDI1.
DR GO; GO:0005829; C:cytosol; IDA.
DR GO; GO:0005094; F:Rho GDP-dissociation inhibitor activity; IDA.
DR GO; GO:0004871; F:signal transducer activity; IPI.
DR GO; GO:0007015; P:actin filament organization; IDA.
DR GO; GO:0007264; P:small GTPase mediated signal transduction; IPI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR000406; Rho_GDI.
DR Pfam; PF02115; Rho_GDI; 1.
DR PRINTS; PR00492; RHOGDI.
KW GTPase activation.
SQ SEQUENCE 202 AA; 23138 MW; 300FF974383B496F CRC64;

Query Match 62.5%; Score 5; DB 1; Length 202;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 NLDAE 7
| | | | |
Db 33 NLDAE 37

RESULT 24

RGS4_HUMAN

ID RGS4_HUMAN STANDARD; PRT; 205 AA.
AC P49798;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Regulator of G-protein signaling 4 (RGS4) (RGP4).
GN RGS4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96178495; PubMed=8602223;
RA Druey K.M., Blumer K.J., Kang V.H., Kehrl J.H.;
RT "Inhibition of G-protein-mediated MAP kinase activation by a new
RT mammalian gene family.";
RL Nature 379:742-746(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain, and Uterus;
RA Puhl H.L. III, Ikeda S.R., Aronstam R.S.;
RT "cDNA clones of human proteins involved in signal transduction
RT sequenced by the Guthrie cDNA resource center (www.cdna.org).";

RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]
 RP PALMITOYLATION.
 RX MEDLINE=20076507; PubMed=10608901;
 RA Tu Y., Popov S., Slaughter C., Ross E.M.;
 RT "Palmitoylation of a conserved cysteine in the regulator of G protein
 RT signaling (RGS) domain modulates the GTPase-activating activity of
 RT RGS4 and RGS10.";
 RL J. Biol. Chem. 274:38260-38267(1999).
 RN [5]
 RP INHIBITION.
 RX MEDLINE=98421527; PubMed=9748280;
 RA Wang J., Ducret A., Tu Y., Kozasa T., Aebersold R., Ross E.M.;
 RT "RGS21, a Gz-selective RGS protein in brain. Structure, membrane
 RT association, regulation by Galphaz phosphorylation, and relationship
 RT to a Gz GTPase-activating protein subfamily.";
 RL J. Biol. Chem. 273:26014-26025(1998).
 CC -!- FUNCTION: INHIBITS SIGNAL TRANSDUCTION BY INCREASING THE GTPASE
 CC ACTIVITY OF G PROTEIN ALPHA SUBUNITS THEREBY DRIVING THEM INTO
 CC THEIR INACTIVE GDP-BOUND FORM. ACTIVITY ON G(Z)-ALPHA IS INHIBITED
 CC BY PHOSPHORYLATION OF THE G-PROTEIN. ACTIVITY ON G(Z)-ALPHA AND
 CC G(I)-ALPHA-1 IS INHIBITED BY PALMITOYLATION OF THE G-PROTEIN.
 CC -!- PTM: Either Cys-2 or Cys-12 or both are palmitoylated.
 CC -!- PTM: Phosphorylated by cyclic GMP-dependent protein kinase (By
 CC similarity).
 CC -!- SIMILARITY: Contains 1 RGS domain.
 CC -----
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CC -----

DR EMBL; U27768; AAC50395.1; -.

DR EMBL; AF493928; AAM12642.1; -.

DR EMBL; BC000737; AAH00737.1; -.

DR EMBL; BC051869; AAH51869.1; -.

DR PIR; S78221; S78221.

DR HSSP; P49799; 1AGR.

DR Genew; HGNC:10000; RGS4.

DR MIM; 602516; -.

DR GO; GO:0005516; F:calmodulin binding; TAS.

DR GO; GO:0005096; F:GTPase activator activity; TAS.

DR GO; GO:0000188; P:inactivation of MAPK; TAS.

DR GO; GO:0008277; P:regulation of G-protein coupled receptor pr. . .; TAS.

DR InterPro; IPR000342; Regl_Gprotein.

DR Pfam; PF00615; RGS; 1.

DR PRINTS; PR01301; RGSPROTEIN.

DR ProDom; PD001580; Regl_Gprotein; 1.

DR SMART; SM00315; RGS; 1.

DR PROSITE; PS50132; RGS; 1.

KW Signal transduction inhibitor; Lipoprotein; Palmitate;

KW Phosphorylation.

FT DOMAIN 62 178 RGS.

FT LIPID 2 2 S-palmitoyl cysteine (Probable).

FT LIPID 12 12 S-palmitoyl cysteine (Probable).

FT LIPID 95 95 S-palmitoyl cysteine.

SQ SEQUENCE 205 AA; 23255 MW; 7713F1F7496A698B CRC64;

Query Match 62.5%; Score 5; DB 1; Length 205;

Best Local Similarity 100.0%; Pred. No. 80;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLD 5

|||||

Db 126 EVNLD 130

RESULT 25

RGS4_MOUSE

ID RGS4_MOUSE STANDARD; PRT; 205 AA.

AC O08899; Q99L30;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Regulator of G-protein signaling 4 (RGS4).

GN RGS4.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6; TISSUE=Substantia nigra;

RX MEDLINE=98086343; PubMed=9425263;

RA Nomoto S., Adachi K., Yang L.X., Hirata Y., Muraguchi S., Kiuchi K.;

RT "Distribution of RGS4 mRNA in mouse brain shown by in situ

RT hybridization.";

RL Biochem. Biophys. Res. Commun. 241:281-287(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Breast tumor;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: INHIBITS SIGNAL TRANSDUCTION BY INCREASING THE GTPASE
 CC ACTIVITY OF G PROTEIN ALPHA SUBUNITS THEREBY DRIVING THEM INTO
 CC THEIR INACTIVE GDP-BOUND FORM. ACTIVITY ON G(Z)-ALPHA IS INHIBITED
 CC BY PHOSPHORYLATION OF THE G-PROTEIN. ACTIVITY ON G(Z)-ALPHA AND
 CC G(I)-ALPHA-1 IS INHIBITED BY PALMITOYLATION OF THE G-PROTEIN (BY
 CC SIMILARITY).
 CC -!- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN BRAIN, MODERATELY
 CC LOW LEVELS IN HEART, AND VERY LOW LEVELS IN LUNG, LIVER, AND
 CC SKELETAL MUSCLE.
 CC -!- PTM: Either Cys-2 or Cys-12 or both are palmitoylated (By
 CC similarity).
 CC -!- PTM: Phosphorylated by cyclic GMP-dependent protein kinase (By
 CC similarity).
 CC -!- SIMILARITY: Contains 1 RGS domain.
 CC -----
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 CC -----
 DR EMBL; AB004315; BAA20400.1; -.
 DR EMBL; BC003882; AAH03882.1; -.
 DR HSSP; P49799; IAGR.
 DR MGD; MGI:108409; Rgs4.
 DR InterPro; IPR000342; Regl_Gprotein.
 DR Pfam; PF00615; RGS; 1.
 DR PRINTS; PR01301; RGSPROTEIN.
 DR ProDom; PD001580; Regl_Gprotein; 1.
 DR SMART; SM00315; RGS; 1.

DR PROSITE; PS50132; RGS; 1.
 KW Signal transduction inhibitor; Lipoprotein; Palmitate;
 KW Phosphorylation.
 FT DOMAIN 62 178 RGS.
 FT LIPID 2 2 S-palmitoyl cysteine (By similarity).
 FT LIPID 12 12 S-palmitoyl cysteine (By similarity).
 FT LIPID 95 95 S-palmitoyl cysteine (By similarity).
 FT CONFLICT 162 162 R -> K (IN REF. 2).
 SQ SEQUENCE 205 AA; 23288 MW; 5D79581711A1F67C CRC64;

Query Match 62.5%; Score 5; DB 1; Length 205;
 Best Local Similarity 100.0%; Pred. No. 80;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLD 5
 |||||
 Db 126 EVNLD 130

RESULT 26

RGS4_RAT

ID RGS4_RAT STANDARD; PRT; 205 AA.
 AC P49799;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Regulator of G-protein signaling 4 (RGS4) (RGP4).
 GN RGS4.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96178495; PubMed=8602223;
 RA Druey K.M., Blumer K.J., Kang V.H., Kehrl J.H.;
 RT "Inhibition of G-protein-mediated MAP kinase activation by a new
 RT mammalian gene family."
 RL Nature 379:742-746(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RA Zhou M.-Y., Gomez-Sanchez C.E., Gomez-Sanchez E.P.;
 RT "The complete cDNA sequence analysis of the rat RGS4."
 RL Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE OF 93-159 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=96140645; PubMed=8548815;
 RA Koelle M.R., Horvitz H.R.;
 RT "EGL-10 regulates G protein signaling in the C. elegans nervous
 RT system and shares a conserved domain with many mammalian proteins."
 RL Cell 84:115-125(1996).
 RN [4]
 RP PHOSPHORYLATION.
 RX MEDLINE=20167219; PubMed=10702309;
 RA Pedram A., Razandi M., Kehrl J., Levin E.R.;

RT "Natriuretic peptides inhibit G protein activation. Mediation through
 RT cross-talk between cyclic GMP-dependent protein kinase and regulators
 RT of G protein-signaling proteins.";
 RL J. Biol. Chem. 275:7365-7372(2000).
 RN [5]
 RP INHIBITION.
 RX MEDLINE=98016286; PubMed=9353196;
 RA Tu Y., Wang J., Ross E.M.;
 RT "Inhibition of brain Gz GAP and other RGS proteins by palmitoylation
 RT of G protein alpha subunits.";
 RL Science 278:1132-1135(1997).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF COMPLEX WITH G(I)-ALPHA.
 RX MEDLINE=97262066; PubMed=9108480;
 RA Tesmer J.J.G., Berman D.M., Gilman A.G., Sprang S.R.;
 RT "Structure of RGS4 bound to AlF4-activated G(i alpha):
 RT stabilization of the transition state for GTP hydrolysis.";
 RL Cell 89:251-261(1997).
 CC -!- FUNCTION: INHIBITS SIGNAL TRANSDUCTION BY INCREASING THE GTPASE
 CC ACTIVITY OF G PROTEIN ALPHA SUBUNITS THEREBY DRIVING THEM INTO
 CC THEIR INACTIVE GDP-BOUND FORM. ACTIVITY ON G(Z)-ALPHA IS INHIBITED
 CC BY PHOSPHORYLATION OF THE G-PROTEIN. ACTIVITY ON G(Z)-ALPHA AND
 CC G(I)-ALPHA-1 IS INHIBITED BY PALMITOYLATION OF THE G-PROTEIN.
 CC -!- PTM: Either Cys-2 or Cys-12 or both are palmitoylated (By
 CC similarity).
 CC -!- PTM: Phosphorylated by cyclic GMP-dependent protein kinase.
 CC -!- SIMILARITY: Contains 1 RGS domain.
 CC -----
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; U27767; AAC52440.1; -.
 DR EMBL; AF117211; AAD12065.1; -.
 DR EMBL; U32327; AAC52367.1; -.
 DR PDB; 1AGR; 16-JUN-97.
 DR PDB; 1EZT; 15-JAN-01.
 DR PDB; 1EZY; 15-JAN-01.
 DR InterPro; IPR000342; Regl_Gprotein.
 DR Pfam; PF00615; RGS; 1.
 DR PRINTS; PR01301; RGSPROTEIN.
 DR ProDom; PD001580; Regl_Gprotein; 1.
 DR SMART; SM00315; RGS; 1.
 DR PROSITE; PS50132; RGS; 1.
 KW Signal transduction inhibitor; Lipoprotein; Palmitate;
 KW Phosphorylation; 3D-structure.
 FT DOMAIN 62 178 RGS.
 FT LIPID 2 2 S-palmitoyl cysteine (By similarity).
 FT LIPID 12 12 S-palmitoyl cysteine (By similarity).
 FT LIPID 95 95 S-palmitoyl cysteine (By similarity).
 FT HELIX 53 59
 FT TURN 60 61
 FT HELIX 63 68

FT	HELIX	70	82
FT	TURN	83	84
FT	TURN	86	86
FT	HELIX	87	100
FT	TURN	104	106
FT	HELIX	107	118
FT	TURN	119	119
FT	TURN	121	122
FT	TURN	124	125
FT	HELIX	131	140
FT	TURN	141	142
FT	TURN	146	149
FT	HELIX	150	162
FT	TURN	163	163
FT	HELIX	164	168
FT	TURN	169	170
FT	HELIX	172	175
FT	TURN	176	176
SQ	SEQUENCE	205 AA;	23248 MW; 9647C0EC909D0F6F CRC64;

Query Match 62.5%; Score 5; DB 1; Length 205;
 Best Local Similarity 100.0%; Pred. No. 80;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLD 5
 |||||
 Db 126 EVNLD 130

RESULT 27

NFNB_ECOLI

ID NFNB_ECOLI STANDARD; PRT; 217 AA.
 AC P38489; P19575;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Oxygen-insensitive NAD(P)H nitroreductase (EC 1.-.-.-) (FMN-dependent
 DE nitroreductase) (Dihydropteridine reductase) (EC 1.6.99.7).
 GN NFNB OR NFSI OR NFSB OR NTR OR DPRA OR B0578.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / C600;
 RA Zenno S., Koike H., Tanokura M., Saigo K.;
 RL Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B;
 RX MEDLINE=95113294; PubMed=7813889;
 RA Michael N.P., Brehm J.K., Anlezark G.M., Minton N.P.;
 RT "Physical characterisation of the Escherichia coli B gene encoding
 RT nitroreductase and its over-expression in Escherichia coli K12."
 RL FEMS Microbiol. Lett. 124:195-202(1994).
 RN [3]

RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1453-1474(1997).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Chung E., Allen E., Araujo R., Aparicio A., Davis K., Duncan M.,
 RA Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew H., Lin D.,
 RA Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=97061202; PubMed=8905232;
 RA Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
 RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
 RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
 RA Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
 RA Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
 RA Yano M., Horiuchi T.;
 RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome
 RT corresponding to the 12.7-28.0 min region on the linkage map.";
 RL DNA Res. 3:137-155(1996).
 RN [6]
 RP CHARACTERIZATION, AND SEQUENCE OF 1-31 AND 139-180.
 RC STRAIN=B;
 RX MEDLINE=93112106; PubMed=1472094;
 RA Anlezark G.M., Melton R.G., Sherwood R.F., Coles B., Friedlos F.,
 RA Knox R.J.;
 RT "The bioactivation of 5-(aziridin-1-yl)-2,4-dinitrobenzamide
 RT (CB1954) -- I. Purification and properties of a nitroreductase enzyme
 RT from Escherichia coli -- a potential enzyme for antibody-directed
 RT enzyme prodrug therapy (ADEPT).";
 RL Biochem. Pharmacol. 44:2289-2295(1992).
 RN [7]
 RP SEQUENCE OF 1-12.
 RC STRAIN=K12 / EMG2;
 RX MEDLINE=97443975; PubMed=9298646;
 RA Link A.J., Robison K., Church G.M.;
 RT "Comparing the predicted and observed properties of proteins encoded
 RT in the genome of Escherichia coli K-12.";
 RL Electrophoresis 18:1259-1313(1997).
 RN [8]
 RP SEQUENCE OF 1-20, AND CHARACTERIZATION AS A DIHYDROPTERIDINE REDUCT.
 RX MEDLINE=89076221; PubMed=3060113;
 RA Vasudevan S.G., Shaw D.C., Armarego W.L.F.;
 RT "Dihydropteridine reductase from Escherichia coli.";
 RL Biochem. J. 255:581-588(1988).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.06 ANGSTROMS).
 RC STRAIN=B;
 RX MEDLINE=20476666; PubMed=11020276;

RA Parkinson G.N., Skelly J.V., Neidle S.;
 RT "Crystal structure of FMN-dependent nitroreductase from Escherichia
 RT coli B: a prodrug-activating enzyme.";
 RL J. Med. Chem. 43:3624-3631(2000).
 CC -!- FUNCTION: REDUCTION OF A VARIETY OF NITROAROMATIC COMPOUNDS USING
 CC NADH (AND TO LESSER EXTENT NADPH) AS SOURCE OF REDUCING
 CC EQUIVALENTS; TWO ELECTRONS ARE TRANSFERRED. CAPABLE OF
 CC NITROFURAZONE, QUINONES AND THE ANTI-TUMOR AGENT CB1954 (5-
 CC (AZIRIDIN-1-YL)-2,4-DINITROBENZAMIDE). THE REDUCTION OF CB1954
 CC RESULTS IN THE GENERATION OF CYTOTOXIC SPECIES.
 CC -!- CATALYTIC ACTIVITY: NAD(P)H + 6,7-dihydropteridine = NAD(P)(+) +
 CC 5,6,7,8-tetrahydropteridine.
 CC -!- COFACTOR: FMN.
 CC -!- SUBUNIT: Monomer or homodimer.
 CC -!- SIMILARITY: Belongs to the nitroreductase family.
 CC -----
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 CC -----
 DR EMBL; D25414; BAA05004.1; -.
 DR EMBL; U07860; AAC43263.1; -.
 DR EMBL; AE000163; AAC73679.1; -.
 DR EMBL; U82598; AAB40776.1; -.
 DR EMBL; D90700; BAA35218.1; -.
 DR EMBL; A23284; CAA01666.1; -.
 DR PIR; I67685; I67685.
 DR PIR; S01818; S01818.
 DR PDB; 1DS7; 12-JUL-00.
 DR PDB; 1ICR; 23-MAY-01.
 DR PDB; 1ICU; 23-MAY-01.
 DR PDB; 1ICV; 23-MAY-01.
 DR SWISS-2DPAGE; P38489; COLI.
 DR EcoGene; EG20151; nfnB.
 DR InterPro; IPR000415; Nitroreductase.
 DR Pfam; PF00881; Nitroreductase; 1.
 KW Oxidoreductase; NAD; NADP; Flavoprotein; FMN; Complete proteome;
 KW 3D-structure.
 FT NP_BIND 153 158 NAD OR NADP (BY SIMILARITY).
 FT CONFLICT 5 5 S -> C (IN REF. 8).
 FT CONFLICT 10 12 RHS -> CIV (IN REF. 8).
 FT CONFLICT 19 19 S -> M (IN REF. 8).
 FT CONFLICT 21 21 MISSING (IN REF. 6).
 FT CONFLICT 28 28 E -> D (IN REF. 6).
 FT CONFLICT 180 180 E -> I (IN REF. 6).
 FT HELIX 3 9
 FT STRAND 12 12
 FT STRAND 16 16
 FT TURN 18 19
 FT HELIX 24 35
 FT TURN 36 36
 FT HELIX 40 42
 FT STRAND 46 51

FT	HELIX	54	61
FT	TURN	62	63
FT	HELIX	66	71
FT	HELIX	72	77
FT	STRAND	80	87
FT	HELIX	92	104
FT	TURN	105	106
FT	HELIX	111	129
FT	TURN	130	132
FT	HELIX	135	157
FT	TURN	158	158
FT	STRAND	160	161
FT	STRAND	164	164
FT	HELIX	169	175
FT	TURN	176	177
FT	HELIX	179	181
FT	TURN	182	182
FT	STRAND	183	192
FT	STRAND	194	194
FT	TURN	196	197
FT	HELIX	199	201
FT	TURN	202	202
FT	HELIX	210	213
FT	STRAND	214	217
SQ	SEQUENCE	217 AA;	23905 MW; A516CEFC3D46AEAC CRC64;

Query Match 62.5%; Score 5; DB 1; Length 217;
 Best Local Similarity 100.0%; Pred. No. 83;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LDAEF 8
 |||||
 Db 172 LDAEF 176

RESULT 28

NFNB_SALTY

ID NFNB_SALTY STANDARD; PRT; 217 AA.
 AC P15888;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Oxygen-insensitive NAD(P)H nitroreductase (EC 1.-.-.-).
 GN NFNB OR NFSI OR STM0578.
 OS Salmonella typhimurium.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Salmonella.
 OX NCBI_TaxID=602;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TA1538;
 RX MEDLINE=90192100; PubMed=2179862;
 RA Watanabe M., Ishidate M., Nohmi T.;
 RT "Nucleotide sequence of Salmonella typhimurium nitroreductase gene."
 RL Nucleic Acids Res. 18:1059-1059(1990).
 RN [2]
 RP SEQUENCE FROM N.A.

Db

18 EVNLD 22

RESULT 13

T37632

hypothetical protein SPAC13F5.07c - fission yeast (*Schizosaccharomyces pombe*)

C;Species: *Schizosaccharomyces pombe*

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 04-Mar-2000

C;Accession: T37632

R;Brown, D.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, September 1997

A;Reference number: Z21733

A;Accession: T37632

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-105 <BRO>

A;Cross-references: EMBL:Z99091; PIDN:CAB11770.1; GSPDB:GN00066;
SPDB:SPAC13F5.07c

A;Experimental source: strain 972h-; cosmid c13F5

C;Genetics:

A;Gene: SPDB:SPAC13F5.07c

A;Map position: 1

C;Superfamily: *Schizosaccharomyces pombe* hypothetical protein SPAC13F5.07c

Query Match 62.5%; Score 5; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LDAEF 8
 |||||
Db 91 LDAEF 95

RESULT 14

S65003

hypothetical protein YLR154c - yeast (*Saccharomyces cerevisiae*)

N;Alternate names: hypothetical protein L3341

C;Species: *Saccharomyces cerevisiae*

C;Date: 01-Aug-1995 #sequence_revision 24-May-1996 #text_change 19-Apr-2002

C;Accession: S65003; S66535

R;Rieger, M.; Mueller-Auer, S.; Brueckner, M.

submitted to the Protein Sequence Database, May 1996

A;Reference number: S64987

A;Accession: S65003

A;Molecule type: DNA

A;Residues: 1-110 <RIE>

A;Cross-references: EMBL:Z73326; NID:g1360587; PIDN:CAA97726.1; PID:g1360588;
MIPS:YLR154c

A;Experimental source: strain S288C

R;van den Berg, M.A.; Steensma, H.Y.

Eur. J. Biochem. 231, 704-713, 1995

A;Title: ACS2, a *Saccharomyces cerevisiae* gene encoding acetyl-coenzyme A
synthetase, essential for growth on glucose.

A;Reference number: S66534; MUID:95377302; PMID:7649171

A;Accession: S66535

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-110 <VAN>
A;Cross-references: EMBL:S79456; NID:g1168013; PIDN:AAB35144.1; PID:g1683551
C;Genetics:
A;Cross-references: SGD:S0004144
A;Map position: 12R
A;Note: YLR154c
C;Superfamily: Saccharomyces hypothetical protein YLR154c

Query Match 62.5%; Score 5; DB 2; Length 110;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VNLDA 6
|||||
Db 6 VNLDA 10

RESULT 15

F83714

holo-(acyl carrier protein) synthase BH0518 [imported] - Bacillus halodurans
(strain C-125)

C;Species: Bacillus halodurans

C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001

C;Accession: F83714

R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji,
F.; Hiramata, C.; Nakamura, Y.; Ogasawara, N.; Kuhara, S.; Horikoshi, K.

Nucleic Acids Res. 28, 4317-4331, 2000

A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus
halodurans and genomic sequence comparison with Bacillus subtilis.

A;Reference number: A83650; MUID:20512582; PMID:11058132

A;Accession: F83714

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-119 <STO>

A;Cross-references: GB:AP001508; GB:BA000004; NID:g10172890; PIDN:BAB04237.1;

GSPDB:GN00137

A;Experimental source: strain C-125

C;Genetics:

A;Gene: BH0518

C;Superfamily: holo-ACP synthase

Query Match 62.5%; Score 5; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VNLDA 6
|||||
Db 91 VNLDA 95

RESULT 16

T18655

hypothetical protein B0035.4 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jul-2000

C;Accession: T18655

R;White, S.

submitted to the EMBL Data Library, May 1996
A;Reference number: Z19002
A;Accession: T18655
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-126 <WIL>
A;Cross-references: EMBL:Z73102; PIDN:CAA97410.1; GSPDB:GN00022; CESP:B0035.4
A;Experimental source: clone B0035
C;Genetics:
A;Gene: CESP:B0035.4
A;Map position: 4
A;Introns: 29/3; 73/3
C;Superfamily: Arabidopsis thaliana hypothetical protein F22013.29

Query Match 62.5%; Score 5; DB 2; Length 126;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 NLDAE 7
| | | | |
Db 121 NLDAE 125

RESULT 17

AH1425

hypothetical secreted protein lmo2809 [imported] - *Listeria monocytogenes*
(strain EGD-e)

C;Species: *Listeria monocytogenes*

C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001

C;Accession: AH1425

R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, H.; Brandt, P.; Chakraborty, T.; Charbit, A.; Chetouani, F.; Couve, E.; de Daruvar, A.; Dehoux, P.; Domann, E.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Garcia-Del Portillo, F.; Garrido, P.; Gautier, L.; Goebel, W.; Gomez-Lopez, N.; Hain, T.; Hauf, J.; Jackson, D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mata Vicente, J.; Ng, E.; Nordsiek, G.; Novella, S.; de Pablos, B.; Perez-Diaz, J.C.; Rimmel, B.; Rose, M.; Rusniok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, J.; Cossart, P.

A;Title: Comparative genomics of *Listeria* species.

A;Reference number: AB1077; MUID:21537279; PMID:11679669

A;Accession: AH1425

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-126 <GLA>

A;Cross-references: GB:NC_003210; PIDN:CAD01022.1; PID:g16412309; GSPDB:GN00177

A;Experimental source: strain EGD-e

C;Genetics:

A;Gene: lmo2809

Query Match 62.5%; Score 5; DB 2; Length 126;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 NLDAE 7

Db |||||
53 NLDAE 57

RESULT 18

H69419

arsenate reductase (arsC) homolog - *Archaeoglobus fulgidus*

C;Species: *Archaeoglobus fulgidus*

C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999

C;Accession: H69419

R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, R.J.; Gwinn, M.; Hickey, E.K.; Peterson, J.D.; Richardson, D.L.; Kerlavage, A.R.; Graham, D.E.; Kyrpides, N.C.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.; Dougherty, B.A.; McKenny, K.; Adams, M.D.; Loftus, B.; Peterson, S.; Reich, C.I.; McNeil, L.K.; Badger, J.H.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.

Nature 390, 364-370, 1997

A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.M.; Sadow, P.W.; D'Andrea, K.P.; Bowman, C.; Fujii, C.; Garland, S.A.; Mason, T.M.; Olsen, G.J.; Fraser, C.M.; Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeon *Archaeoglobus fulgidus*.

A;Reference number: A69250; MUID:98049343; PMID:9389475

A;Accession: H69419

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-135 <KLE>

A;Cross-references: GB:AE001010; GB:AE000782; NID:g2689333; PIDN:AAB89885.1; PID:g2649214; TIGR:AF1361

C;Superfamily: protein-tyrosine-phosphatase, low molecular weight

Query Match 62.5%; Score 5; DB 2; Length 135;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLD 5
 |||||
Db 65 EVNLD 69

RESULT 19

H72633

hypothetical protein APE1527 - *Aeropyrum pernix* (strain K1)

C;Species: *Aeropyrum pernix*

C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000

C;Accession: H72633

R;Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahashi, M.; Sekine, M.; Baba, S.; Ankai, A.; Kosugi, H.; Hosoyama, A.; Fukui, S.; Nagai, Y.; Nishijima, K.; Nakazawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi, A.; Aoki, K.; Kubota, K.; Nakamura, Y.; Nomura, N.; Sako, Y.; Kikuchi, H.

DNA Res. 6, 83-101, 1999

A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, *Aeropyrum pernix* K1.

A;Reference number: A72450; MUID:99310339; PMID:10382966

A;Accession: H72633

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-136 <KAW>
A;Cross-references: DDBJ:AP000061; NID:g5104821; PIDN:BAA80526.1; PID:g5105212
A;Experimental source: strain K1
C;Genetics:
A;Gene: APE1527
C;Superfamily: Aeropyrum pernix hypothetical protein APE1527

Query Match 62.5%; Score 5; DB 2; Length 136;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 NLDAE 7
| | | |
Db 29 NLDAE 33

RESULT 20

S77399

urease accessory protein E - Synechocystis sp. (strain PCC 6803)
N;Alternate names: protein slr1219
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 28-Jul-2003
C;Accession: S77399
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.;
Miyajima, N.; Hirose, M.; Sugiura, M.; Sasamoto, S.; Kimura, T.; Hosouchi, T.;
Matsuno, A.; Muraki, A.; Nakazaki, N.; Naruo, K.; Okumura, S.; Shimpo, S.;
Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium
Synechocystis sp. PCC6803. II. Sequence determination of the entire genome and
assignment of potential protein-coding regions.
A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S77399
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-142 <KAN>
A;Cross-references: EMBL:D90906; GB:AB001339; NID:g1652492; PIDN:BAA17502.1;
PID:d1018235; PID:g1652581
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June
1996
C;Genetics:
A;Gene: ureE
C;Superfamily: urease accessory protein (nickel metallochaperone), UreE type

Query Match 62.5%; Score 5; DB 2; Length 142;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLD 5
| | | |
Db 100 EVNLD 104

RESULT 21

B83069

hypothetical protein PA4610 [imported] - *Pseudomonas aeruginosa* (strain PAO1)

C;Species: *Pseudomonas aeruginosa*

C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C;Accession: B83069

R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Brinkman, F.S.L.; Hufnagle, W.O.; Kowalik, D.J.; Lagrou, M.; Garber, R.L.; Goltry, L.; Tolentino, E.; Westbrook-Wadman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, R.M.; Smith, K.A.; Spencer, D.H.; Wong, G.K.S.; Wu, Z.; Paulsen, I.T.; Reizer, J.; Saier, M.H.; Hancock, R.E.W.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A;Title: Complete genome sequence of *Pseudomonas aeruginosa* PAO1, an opportunistic pathogen.

A;Reference number: A82950; MUID:20437337; PMID:10984043

A;Accession: B83069

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-144 <STO>

A;Cross-references: GB:AE004875; GB:AE004091; NID:g9950857; PIDN:AAG07998.1; GSPDB:GN00131; PASP:PA4610

A;Experimental source: strain PAO1

C;Genetics:

A;Gene: PA4610

Query Match 62.5%; Score 5; DB 2; Length 144;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 NLDAE 7
| | | | |
Db 108 NLDAE 112

RESULT 22

S75581

hypothetical protein sl10802 - *Synechocystis* sp. (strain PCC 6803)

C;Species: *Synechocystis* sp.

A;Variety: PCC 6803

C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000

C;Accession: S75581

R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; Hirosawa, M.; Sugiura, M.; Sasamoto, S.; Kimura, T.; Hosouchi, T.; Matsuno, A.; Muraki, A.; Nakazaki, N.; Naruo, K.; Okumura, S.; Shimpō, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 3, 109-136, 1996

A;Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis* sp. PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.

A;Reference number: S74322; MUID:97061201; PMID:8905231

A;Accession: S75581

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-147 <KAN>

A;Cross-references: EMBL:D90911; GB:AB001339; NID:g1653083; PIDN:BAA18142.1; PID:g1653226

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C;Superfamily: hypothetical protein slr1203

Query Match 62.5%; Score 5; DB 2; Length 147;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LDAEF 8
|||||
Db 140 LDAEF 144

RESULT 23

AH1166

ribose 5-phosphate isomerase homolog lmo0736 [imported] - *Listeria monocytogenes* (strain EGD-e)

C;Species: *Listeria monocytogenes*

C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001

C;Accession: AH1166

R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, H.; Brandt, P.; Chakraborty, T.; Charbit, A.; Chetouani, F.; Couve, E.; de Daruvar, A.; Dehoux, P.; Domann, E.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Garcia-Del Portillo, F.; Garrido, P.; Gautier, L.; Goebel, W.; Gomez-Lopez, N.; Hain, T.; Hauf, J.; Jackson, D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mata Vicente, J.; Ng, E.; Nordsiek, G.; Novella, S.; de Pablos, B.; Perez-Diaz, J.C.; Rimmel, B.; Rose, M.; Rusniok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, J.; Cossart, P.

A;Title: Comparative genomics of *Listeria* species.

A;Reference number: AB1077; MUID:21537279; PMID:11679669

A;Accession: AH1166

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-148 <GLA>

A;Cross-references: GB:NC_003210; PIDN:CAC98814.1; PID:g16410125; GSPDB:GN00177

A;Experimental source: strain EGD-e

C;Genetics:

A;Gene: lmo0736

C;Superfamily: galactoside O-acetyltransferase

Query Match 62.5%; Score 5; DB 2; Length 148;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LDAEF 8
|||||
Db 124 LDAEF 128

RESULT 24

AC0407

ribose-5-phosphate isomerase (EC 5.3.1.6) [imported] - *Yersinia pestis* (strain CO92)

C;Species: *Yersinia pestis*

C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001
 C;Accession: AC0407
 R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.;
 Prentice, M.B.; Sebahia, M.; James, K.D.; Churcher, C.; Mungall, K.L.; Baker,
 S.; Basham, D.; Bentley, S.D.; Brooks, K.; Cerdeno-Tarraga, A.M.; Chillingworth,
 T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Feltwell, T.; Hamlin, N.;
 Holroyd, S.; Jagels, K.; Leather, S.; Karlyshev, A.V.; Moule, S.; Oyston,
 P.C.F.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
 Whitehead, S.; Barrell, B.G.
 Nature 413, 523-527, 2001
 A;Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.
 A;Reference number: AB0001; MUID:21470413; PMID:11586360
 A;Accession: AC0407
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-151 <KUR>
 A;Cross-references: GB:AL590842; PIDN:CAC92583.1; PID:g15981280; GSPDB:GN00175
 C;Genetics:
 A;Gene: rpiB
 C;Superfamily: galactoside O-acetyltransferase
 C;Keywords: intramolecular oxidoreductase; isomerase

Query Match 62.5%; Score 5; DB 2; Length 151;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LDAEF 8
 |||||
 Db 126 LDAEF 130

RESULT 25
 B70800
 hypothetical protein Rv3753c - *Mycobacterium tuberculosis* (strain H37RV)
 C;Species: *Mycobacterium tuberculosis*
 C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
 C;Accession: B70800
 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.;
 Gordon, S.V.; Eiglmeier, K.; Gas, S.; Barry III, C.E.; Tekaia, F.; Badcock, K.;
 Basham, D.; Brown, D.; Chillingworth, T.; Connor, R.; Davies, R.; Devlin, K.;
 Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Hornsby, T.; Jagels, K.;
 Krogh, A.; McLean, J.; Moule, S.; Murphy, L.; Oliver, S.; Osborne, J.; Quail,
 M.A.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.;
 Squares, S.
 Nature 393, 537-544, 1998
 A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A;Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete
 genome sequence.
 A;Reference number: A70500; MUID:98295987; PMID:9634230
 A;Accession: B70800
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-166 <COL>
 A;Cross-references: GB:AL022121; GB:AL123456; NID:g3261559; PIDN:CAA18075.1;
 PID:e1264613; PID:g2960177
 A;Experimental source: strain H37Rv
 C;Genetics:

A;Gene: Rv3753c

Query Match 62.5%; Score 5; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 NLDAE 7
|||||
Db 95 NLDAE 99

RESULT 26

G82898

conserved hypothetical UU380 [imported] - *Ureaplasma urealyticum*

C;Species: *Ureaplasma urealyticum*

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000

C;Accession: G82898

R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.

submitted to GenBank, February 2000

A;Description: The complete sequence of *Ureaplasma urealyticum*: Alternate views of a minimal genome and sexually transmitted pathogen.

A;Reference number: A82870

A;Accession: G82898

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-168 <GLA>

A;Cross-references: GB:AE002135; GB:AF222894; NID:g6899358; PIDN:AAF30790.1;

GSPDB:GN00123; UUSP:UU380

A;Experimental source: serovar 3; biovar 1

C;Genetics:

A;Gene: UU380

A;Genetic code: SGC3

Query Match 62.5%; Score 5; DB 2; Length 168;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VNLDA 6
|||||
Db 35 VNLDA 39

RESULT 27

T08348

hypothetical protein H1517 [imported] - *Halobacterium* sp. (strain NRC-1) plasmid pNRC100

C;Species: *Halobacterium* sp.

A;Variety: strain NRC-1

C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 03-Nov-2000

C;Accession: T08348

R;Ng, W.V.; Ciufu, S.A.; Smith, T.M.; Bumgarner, R.E.; Baskin, D.; Faust, J.; Hall, B.; Loretz, C.; Seto, J.; Slagel, J.; Hood, L.; DasSarma, S.

Genome Res. 8, 1131-1141, 1998

A;Title: Snapshot of a large dynamic replicon in a halophilic Archaeon: megaplasmid or minichromosome?

A;Reference number: Z16408; MUID:99063795; PMID:9847077

A;Accession: T08348
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-170 <DAS>
A;Cross-references: EMBL:AF016485; NID:g2822278; PID:g2822409; HALOSP:H1517
A;Experimental source: strain NRC-1
C;Genetics:
A;Gene: HALOSP:H1517
A;Genome: plasmid pNRC100

Query Match 62.5%; Score 5; DB 2; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LDAEF 8
| | | |
Db 75 LDAEF 79

RESULT 28

F65038

hypothetical protein b2603 - Escherichia coli (strain K-12)

C;Species: Escherichia coli

C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002

C;Accession: F65038

R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.;
Riley, M.; Collado-Vides, J.; Glasner, J.D.; Rode, C.K.; Mayhew, G.F.; Gregor,
J.; Davis, N.W.; Kirkpatrick, H.A.; Goeden, M.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997

A;Title: The complete genome sequence of Escherichia coli K-12.

A;Reference number: A64720; MUID:97426617; PMID:9278503

A;Accession: F65038

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-172 <BLAT>

A;Cross-references: GB:AE000346; GB:U00096; NID:g2367141; PIDN:AAC75652.1;

PID:gl788955; UWGP:b2603

A;Experimental source: strain K-12, substrain MG1655

C;Superfamily: Escherichia coli hypothetical protein b2603

Query Match 62.5%; Score 5; DB 2; Length 172;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VNLDA 6
| | | |
Db 146 VNLDA 150

RESULT 29

B91062

hypothetical protein ECs3466 [imported] - Escherichia coli (strain O157:H7,
substrain RIMD 0509952)

C;Species: Escherichia coli

C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001

C;Accession: B91062

R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.; Ohtsubo, E.; Nakayama, K.; Murata, T.; Tanaka, M.; Tobe, T.; Iida, T.; Takami, H.; Honda, T.; Sasakawa, C.; Ogasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
 DNA Res. 8, 11-22, 2001
 A;Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and genomic comparison with a laboratory strain K-12.
 A;Reference number: A99629; MUID:21156231; PMID:11258796
 A;Accession: B91062
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-172 <HAY>
 A;Cross-references: GB:BA000007; PIDN:BAB36889.1; PID:g13362937; GSPDB:GN00154
 A;Experimental source: strain O157:H7, substrain RIMD 0509952
 C;Genetics:
 A;Gene: ECs3466
 C;Superfamily: *Escherichia coli* hypothetical protein b2603

Query Match 62.5%; Score 5; DB 2; Length 172;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VNLDA 6
 |||||
 Db 146 VNLDA 150

RESULT 30

F85906

hypothetical protein Z3897 [imported] - *Escherichia coli* (strain O157:H7, substrain EDL933)

C;Species: *Escherichia coli*

C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001

C;Accession: F85906

R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, G.F.; Evans, P.S.; Gregor, J.; Kirkpatrick, H.A.; Posfai, G.; Hackett, J.; Klink, S.; Boutin, A.; Shao, Y.; Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamouisis, K.; Apodaca, J.; Anantharaman, T.S.; Lin, J.; Yen, G.; Schwartz, D.C.; Welch, R.A.; Blattner, F.R.
 Nature 409, 529-533, 2001

A;Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.

A;Reference number: A85480; MUID:21074935; PMID:11206551

A;Accession: F85906

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-172 <STO>

A;Cross-references: GB:AE005174; NID:g12517025; PIDN:AAG57714.1; GSPDB:GN00145; UWGP:Z3897

A;Experimental source: strain O157:H7, substrain EDL933

C;Genetics:

A;Gene: Z3897

C;Superfamily: *Escherichia coli* hypothetical protein b2603

Query Match 62.5%; Score 5; DB 2; Length 172;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VNLDA 6
|||||
Db 146 VNLDA 150

RESULT 31

H81251

NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) I chain J Cj1570c [imported] -
Campylobacter jejuni (strain NCTC 11168)

C;Species: Campylobacter jejuni

C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002

C;Accession: H81251

R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.;
Chillingworth, T.; Davies, R.M.; Feltwell, T.; Holroyd, S.; Jagels, K.;

Karlyshev, A.; Moule, S.; Pallen, M.J.; Penn, C.W.; Quail, M.; Rajandream, M.A.;
Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrell, B.G.

Nature 403, 665-668, 2000

A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni
reveals hypervariable sequences.

A;Reference number: A81250; MUID:20150912; PMID:10688204

A;Accession: H81251

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-172 <PAR>

A;Cross-references: GB:AL139079; GB:AL111168; NID:g6968971; PIDN:CAB73558.1;
PID:g6968987; GSPDB:GN00120; CJSP:Cj1570c

A;Experimental source: serotype O2, strain NCTC 11168

C;Genetics:

A;Gene: nuoJ; Cj1570c

C;Keywords: NAD; oxidoreductase

Query Match 62.5%; Score 5; DB 2; Length 172;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LDAEF 8
|||||
Db 48 LDAEF 52

RESULT 32

S67579

probable membrane protein YDL046w - yeast (Saccharomyces cerevisiae)

N;Alternate names: hypothetical protein D2699

C;Species: Saccharomyces cerevisiae

C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 19-Apr-2002

C;Accession: S67579

R;Paulin, L.; Saren, A.M.; Laamanen, P.

submitted to the Protein Sequence Database, July 1996

A;Reference number: S67560

A;Accession: S67579

A;Molecule type: DNA

A;Residues: 1-173 <PAU>

A;Cross-references: EMBL:Z74094; NID:g1431035; PID:e253204; PID:g1431036;
GSPDB:GN00004; MIPS:YDL046w

A;Experimental source: strain S288C

C;Genetics:

A;Gene: MIPS:YDL046w
A;Cross-references: SGD:S0002204
A;Map position: 4L
C;Superfamily: Saccharomyces cerevisiae probable membrane protein YDL046w
C;Keywords: transmembrane protein
F;8-24/Domain: transmembrane #status predicted <TMM>

Query Match 62.5%; Score 5; DB 2; Length 173;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLD 5
|||||
Db 59 EVNLD 63

RESULT 33

E64678

NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain NQO10 - Helicobacter pylori (strain 26695)

C;Species: Helicobacter pylori

C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 03-Jun-2002

C;Accession: E64678

R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Ketchum, K.A.; Klenk, H.P.; Gill, S.; Dougherty, B.A.; Nelson, K.; Quackenbush, J.; Zhou, L.; Kirkness, E.F.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney, K.; Fitzegerald, L.M.; Lee, N.; Adams, M.D.; Hickey, E.K.; Berg, D.E.; Gocayne, J.D.; Utterback, T.R.; Peterson, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.

Nature 388, 539-547, 1997

A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.M.; Venter, J.C.

A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.

A;Reference number: A64520; MUID:97394467; PMID:9252185

A;Accession: E64678

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-182 <TOM>

A;Cross-references: GB:AE000631; GB:AE000511; NID:g2314421; PIDN:AAD08313.1;

PID:g2314434; TIGR:HP1269

C;Superfamily: NADH dehydrogenase (ubiquinone) chain 6

C;Keywords: electron transfer; membrane-associated complex; NAD; oxidoreductase

Query Match 62.5%; Score 5; DB 2; Length 182;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LDAEF 8
|||||
Db 48 LDAEF 52

RESULT 34

C71839

NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) I chain J - *Helicobacter pylori* (strain J99)

C;Species: *Helicobacter pylori*

A;Variety: strain J99

C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 03-Jun-2002

C;Accession: C71839

R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Noonan, B.; Guild, B.C.; deJonge, B.L.; Carmel, G.; Tummino, P.J.; Caruso, A.; Uria-Nickelsen, M.; Mills, D.M.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Trust, T.J.
Nature 397, 176-180, 1999

A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric pathogen *Helicobacter pylori*.

A;Reference number: A71800; MUID:99120557; PMID:9923682

A;Accession: C71839

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-182 <ARN>

A;Cross-references: GB:AE001545; GB:AE001439; NID:g4155776; PIDN:AAD06756.1; PID:g4155780

A;Experimental source: strain J99

C;Genetics:

A;Gene: nuoJ

C;Superfamily: NADH dehydrogenase (ubiquinone) chain 6

C;Keywords: membrane-associated complex; NAD; oxidoreductase

Query Match 62.5%; Score 5; DB 2; Length 182;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LDAEF 8
|||||
Db 48 LDAEF 52

RESULT 35

AE2330

adenylate kinase [imported] - *Nostoc* sp. (strain PCC 7120)

C;Species: *Nostoc* sp. PCC 7120

A;Note: *Nostoc* sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120

C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002

C;Accession: AE2330

R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, M.; Ishikawa, A.; Kawashima, K.; Kimura, T.; Kishida, Y.; Kohara, M.; Matsumoto, M.; Matsuno, A.; Muraki, A.; Nakazaki, N.; Shimpō, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.

DNA Res. 8, 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Anabaena* sp. strain PCC 7120.

A;Reference number: AB1807; MUID:21595285; PMID:11759840

A;Accession: AE2330

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-184 <KUR>

A;Cross-references: GB:BA000019; PIDN:BA000019.1; PID:g17133331; GSPDB:GN00179

A;Experimental source: strain PCC 7120

C;Genetics:

A;Gene: all4196

C;Superfamily: adenylate kinase

Query Match 62.5%; Score 5; DB 2; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VNLDA 6
|||||
Db 112 VNLDA 116

RESULT 36

S61047

hypothetical protein YDL166c - yeast (*Saccharomyces cerevisiae*)

N;Alternate names: hypothetical protein D1487

C;Species: *Saccharomyces cerevisiae*

C;Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 19-Apr-2002

C;Accession: S61047; S67718

R;Pohl, T.M.

submitted to the EMBL Data Library, November 1995

A;Reference number: S61010

A;Accession: S61047

A;Molecule type: DNA

A;Residues: 1-197 <POH>

A;Cross-references: EMBL:Z67750; NID:g1061256; PIDN:CAA91580.1; PID:g1061273

R;Pohl, T.M.

submitted to the Protein Sequence Database, July 1996

A;Reference number: S67708

A;Accession: S67718

A;Molecule type: DNA

A;Residues: 1-197 <POW>

A;Cross-references: EMBL:Z74214; NID:g1431263; PIDN:CAA98740.1; PID:g1431264;

MIPS:YDL166c

A;Experimental source: strain S288C

C;Genetics:

A;Cross-references: SGD:S0002325

A;Map position: 4L

C;Superfamily: conserved hypothetical protein MJ1050

Query Match 62.5%; Score 5; DB 2; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 NLDAE 7
|||||
Db 124 NLDAE 128

RESULT 37

E64102

skp protein - *Haemophilus influenzae* (strain Rd KW20)

C;Species: *Haemophilus influenzae*

C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 08-Oct-1999

C;Accession: E64102

R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.;

Kerlavage, A.R.; Bult, C.J.; Tomb, J.F.; Dougherty, B.A.; Merrick, J.M.;

McKenney, K.; Sutton, G.; FitzHugh, W.; Fields, C.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.F.; Phillips, C.A.; Spriggs, T.; Hedblom, E.; Cotton, M.D.; Utterback, T.R.; Hanna, M.C.; Nguyen, D.T.; Saudek, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.

Science 269, 496-512, 1995

A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, J.C.

A;Title: Whole-genome random sequencing and assembly of *Haemophilus influenzae* Rd.

A;Reference number: A64000; MUID:95350630; PMID:7542800

A;Accession: E64102

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-197 <TIGR>

A;Cross-references: GB:U32773; GB:L42023; NID:g1573932; PIDN:AAC22574.1;

PID:g1573937; TIGR:HI0916

C;Genetics:

A;Gene: *skp*

Query Match 62.5%; Score 5; DB 2; Length 197;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LDAEF 8

||||

Db 49 LDAEF 53

RESULT 38

AG0986

hypothetical luxR-family transcription regulator STY4197 [imported] - *Salmonella enterica* subsp. *enterica* serovar Typhi (strain CT18)

C;Species: *Salmonella enterica* subsp. *enterica* serovar Typhi

A;Note: this species has also been called *Salmonella typhi*

C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 15-Sep-2003

C;Accession: AG0986

R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, C.; Mungall, K.L.; Bentley, S.D.; Holden, M.T.G.; Sebaihia, M.; Baker, S.; Basham, D.; Brooks, K.; Chillingworth, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, J.; Feltwell, T.; Hamlin, N.; Haque, A.; Hien, T.T.; Holroyd, S.; Jagels, K.; Krogh, A.; Larsen, T.S.; Leather, S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, B.G.

A;Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serovar Typhi CT18.

A;Reference number: AB0502; MUID:21534947; PMID:11677608

A;Accession: AG0986

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-200 <PAR>

A;Cross-references: GB:AL513382; PIDN:CAD08019.1; PID:g16505002; GSPDB:GN00176

C;Genetics:

A;Gene: STY4197

C;Superfamily: response regulator with HTH DNA-binding domain, NarL type;
response regulator homology

Query Match 62.5%; Score 5; DB 2; Length 200;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LDAEF 8
|||||
Db 56 LDAEF 60

RESULT 39

A53646

rho GDP dissociation inhibitor - yeast (*Saccharomyces cerevisiae*)

N;Alternate names: protein D2175; protein YDL135c

C;Species: *Saccharomyces cerevisiae*

C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 18-Aug-2000

C;Accession: A53646; B53646; S67681

R;Masuda, T.; Tanaka, K.; Nonaka, H.; Yamochi, W.; Maeda, A.; Takai, Y.

J. Biol. Chem. 269, 19713-19718, 1994

A;Title: Molecular cloning and characterization of yeast rho GDP dissociation inhibitor.

A;Reference number: A53646; MUID:94327511; PMID:8051050

A;Accession: A53646

A;Molecule type: DNA

A;Residues: 1-202 <MAS>

A;Cross-references: GB:D31630; NID:g516856; PIDN:BAA06499.1; PID:g516857

A;Accession: B53646

A;Molecule type: protein

A;Residues: 27-42;66-70;116-131;140-152;155-163 <MA2>

R;Saluz, H.P.; Woelfl, S.; Hanemann, V.

submitted to the Protein Sequence Database, July 1996

A;Reference number: S67677

A;Accession: S67681

A;Molecule type: DNA

A;Residues: 1-202 <SAL>

A;Cross-references: EMBL:Z74183; NID:g1431206; PID:g1431207; MIPS:YDL135c

A;Experimental source: strain S288C

C;Genetics:

A;Gene: SGD:RDI1

A;Cross-references: SGD:S0002294; MIPS:YDL135c

A;Map position: 4L

C;Superfamily: human rho GDP dissociation inhibitor

Query Match 62.5%; Score 5; DB 2; Length 202;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 NLDAE 7
|||||
Db 33 NLDAE 37

RESULT 40

S78221

G-protein signaling regulator RGP4 - human

N;Alternate names: G-protein signaling regulator RGS4
 C;Species: Homo sapiens (man)
 C;Date: 29-Jan-1998 #sequence_revision 13-Feb-1998 #text_change 31-Jan-2000
 C;Accession: S78221; S68509
 R;Druey, K.
 submitted to the EMBL Data Library, May 1995
 A;Reference number: S78089
 A;Accession: S78221
 A;Molecule type: mRNA
 A;Residues: 1-205 <DRU>
 A;Cross-references: EMBL:U27768; NID:g1216372; PIDN:AAC50395.1; PID:g1216373
 R;Druey, K.M.; Blumer, K.J.; Kang, V.H.; Kehrl, J.H.
 Nature 379, 742-746, 1996
 A;Title: Inhibition of G-protein-mediated MAP kinase activation by a new
 mammalian gene family.
 A;Reference number: A58012; MUID:96178495; PMID:8602223
 A;Accession: S68509
 A;Status: preliminary; nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 1-35,'S',37-39,'S',41-46,'T',48-67,'N',69-76,'L',78-177,'T',179-
 197,'T',199-205 <DRW>
 A;Cross-references: EMBL:U27768
 A;Experimental source: brain
 C;Superfamily: B-cell activation protein BL34

Query Match 62.5%; Score 5; DB 2; Length 205;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLD 5
 |||||
 Db 126 EVNLD 130

Search completed: March 26, 2004, 15:35:56
 Job time : 27.5 secs

RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
 RX MEDLINE=21534948; PubMed=11677609;
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
 RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
 RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
 RA Waterston R., Wilson R.K.;
 RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
 RT LT2.";
 RL Nature 413:852-856(2001).
 CC -!- FUNCTION: REDUCTION OF A VARIETY OF NITROAROMATIC COMPOUNDS USING
 CC NADH (AND TO LESSER EXTENT NADPH) AS SOURCE OF REDUCING
 CC EQUIVALENTS; TWO ELECTRONS ARE TRANSFERRED. CAPABLE OF REDUCING
 CC NITROFURAZONE (BY SIMILARITY).
 CC -!- COFACTOR: FMN.
 CC -!- SUBUNIT: Monomer (By similarity).
 CC -!- SIMILARITY: Belongs to the nitroreductase family.
 CC -----
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 CC -----
 DR EMBL; X17250; CAA35113.1; -.
 DR EMBL; AE008722; AAL19529.1; -.
 DR PIR; S08397; S08397.
 DR HSSP; P38489; 1DS7.
 DR StyGene; SG10246; nfnB.
 DR InterPro; IPR000415; Nitroreductase.
 DR Pfam; PF00881; Nitroreductase; 1.
 KW Oxidoreductase; NAD; NADP; Flavoprotein; FMN; Complete proteome.
 FT NP_BIND 153 158 NAD OR NADP (BY SIMILARITY).
 SQ SEQUENCE 217 AA; 23955 MW; E90E9E05A0826D0F CRC64;

Query Match 62.5%; Score 5; DB 1; Length 217;
 Best Local Similarity 100.0%; Pred. No. 83;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LDAEF 8
 |||||
 Db 172 LDAEF 176

RESULT 29

MINC_PASMU

ID MINC_PASMU STANDARD; PRT; 225 AA.
 AC P57845;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Probable septum site-determining protein minC.
 GN MINC OR PM0443.
 OS Pasteurella multocida.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;

OC Pasteurellaceae; Pasteurella.
 OX NCBI_TaxID=747;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Pm70;
 RX MEDLINE=21145866; PubMed=11248100;
 RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
 RT "Complete genomic sequence of Pasteurella multocida Pm70."
 RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
 CC -!- FUNCTION: Cell division inhibitor that blocks the formation of
 CC polar Z ring septums. Rapidly oscillates between the poles of the
 CC cell to destabilize ftsZ filaments that have formed before they
 CC mature into polar Z rings. Prevent ftsZ polymerization (By
 CC similarity).
 CC -!- SUBUNIT: Interacts with minD and ftsZ (By similarity).
 CC -!- SIMILARITY: Belongs to the minC family.
 CC -----
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 CC -----
 DR EMBL; AE006080; AAK02527.1; -.
 DR HAMAP; MF_00267; -; 1.
 DR InterPro; IPR005526; MinC.
 DR InterPro; IPR007874; MinC_N.
 DR Pfam; PF03775; MinC_C; 1.
 DR Pfam; PF05209; MinC_N; 1.
 DR TIGRFAMs; TIGR01222; minC; 1.
 KW Cell division; Septation; Complete proteome.
 SQ SEQUENCE 225 AA; 25210 MW; B64BB77F802AA58E CRC64;

Query Match 62.5%; Score 5; DB 1; Length 225;
 Best Local Similarity 100.0%; Pred. No. 86;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LDAEF 8
 |||||
 Db 180 LDAEF 184

RESULT 30
 Y127_TREPA
 ID Y127_TREPA STANDARD; PRT; 229 AA.
 AC O83164;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein TP0127.
 GN TP0127.
 OS Treponema pallidum.
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
 OX NCBI_TaxID=160;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=Nichols;
 RX MEDLINE=98332770; PubMed=9665876;
 RA Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
 RA Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
 RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
 RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,
 RA McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S.,
 RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
 RA Venter J.C.;
 RT "Complete genome sequence of *Treponema pallidum*, the syphilis
 RT spirochete."
 RL Science 281:375-388(1998).
 CC -!- SIMILARITY: TO T.PALLIDUM TP0315, TP0618 AND TP0619.
 CC -----
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 CC -----
 DR EMBL; AE001198; AAC65119.1; -.
 DR PIR; D71362; D71362.
 DR TIGR; TP0127; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 229 AA; 24870 MW; 39C216395BC6FE88 CRC64;

Query Match 62.5%; Score 5; DB 1; Length 229;
 Best Local Similarity 100.0%; Pred. No. 87;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VNLDA 6
 |||||
 Db 89 VNLDA 93

RESULT 31

CTRA_CAUCR

ID CTRA_CAUCR STANDARD; PRT; 231 AA.
 AC Q45994;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Cell cycle transcriptional regulator ctrA (Response regulator sokA).
 GN CTRA OR SOKA OR CC3035.
 OS *Caulobacter crescentus*.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
 OC Caulobacteraceae; Caulobacter.
 OX NCBI_TaxID=155892;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CB15N / NA1000;
 RX MEDLINE=96140642; PubMed=8548829;
 RA Quon K.C., Marczyński G.T., Shapiro L.;
 RT "Cell cycle control by an essential bacterial two-component signal

RT transduction protein.";
 RL Cell 84:83-93(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 19089 / CB15;
 RX MEDLINE=21173698; PubMed=11259647;
 RA Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
 RA Eisen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
 RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
 RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
 RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
 RA Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
 RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
 RT "Complete genome sequence of *Caulobacter crescentus*.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
 RN [3]
 RP SEQUENCE OF 159-231 FROM N.A.
 RC STRAIN=ATCC 19089 / CB15;
 RX MEDLINE=98132609; PubMed=9465034;
 RA Wu J., Ohta N., Newton A.;
 RT "An essential, multicomponent signal transduction pathway required for
 RT cell cycle regulation in *Caulobacter*.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:1443-1448(1998).
 CC -!- FUNCTION: FORMS PART OF A TWO-COMPONENT REGULATORY SYSTEM
 CC CTRA/CCKA THAT CONTROLS MULTIPLE EVENTS IN THE CELL CYCLE,
 CC INCLUDING CELL DIVISION, STALK SYNTHESIS, AND CELL CYCLE-SPECIFIC
 CC TRANSCRIPTION. BINDS TO A GROUP OF CELL CYCLE-REGULATED PROMOTERS
 CC CRITICAL FOR DNA REPLICATION, DNA METHYLATION, AND CLASS II
 CC FLAGELLAR BIOGENESIS.
 CC -!- PTM: PHOSPHORYLATED BY CCKA.
 CC -!- SIMILARITY: Contains 1 response regulatory domain.
 CC -----
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 CC -----
 DR EMBL; U39559; AAA93080.1; -.
 DR EMBL; AE005966; AAK24997.1; -.
 DR EMBL; AF021339; AAC05479.1; -.
 DR PIR; A87625; A87625.
 DR HSSP; P08402; 1B00.
 DR TIGR; CC3035; -.
 DR InterPro; IPR001789; Response_reg.
 DR InterPro; IPR001867; Trans_reg_C.
 DR Pfam; PF00072; response_reg; 1.
 DR Pfam; PF00486; trans_reg_C; 1.
 DR ProDom; PD000039; Response_reg; 1.
 DR ProDom; PD000329; Trans_reg_C; 1.
 DR SMART; SM00448; REC; 1.
 DR PROSITE; PS50110; RESPONSE_REGULATORY; 1.
 KW Sensory transduction; Phosphorylation; Transcription regulation;
 KW DNA-binding; Complete proteome.
 FT DOMAIN 1 116 RESPONSE REGULATORY.

FT MOD_RES 51 51 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 231 AA; 25796 MW; BB812AF6EDAADB8 CRC64;

Query Match 62.5%; Score 5; DB 1; Length 231;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VNLDA 6
|
Db 134 VNLDA 138

RESULT 32

RL1_HELPJ

ID RL1_HELPJ STANDARD; PRT; 234 AA.
AC Q9ZK21;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE 50S ribosomal protein L1.
GN RPLA OR JHP1124.
OS Helicobacter pylori J99 (Campylobacter pylori J99).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=85963;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99120557; PubMed=9923682;
RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
RA Trust T.J.;
RT "Genomic sequence comparison of two unrelated isolates of the human
RT gastric pathogen Helicobacter pylori.";
RL Nature 397:176-180(1999).
CC -!- FUNCTION: This protein binds directly to 23S rRNA and is located
CC in the neighborhood of the site where elongation factor Tu is
CC bound to the ribosome (By similarity).
CC -!- FUNCTION: Peptides originating from the N-terminal end of L1 have
CC antibacterial activity against bacteria such as E.coli and
CC B.megaterium. Has no effect on H.pylori itself. These peptides
CC may be released in the stomach during autolysis so as to
CC kill other fast growing bacteria (By similarity).
CC -!- SUBUNIT: Part of the 50S ribosomal subunit.
CC -!- SIMILARITY: Belongs to the L1P family of ribosomal proteins.
CC -----
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CC -----
DR EMBL; AE001540; AAD06702.1; -.
DR PIR; E71846; E71846.

DR HSSP; P27150; 1AD2.
 DR HAMAP; MF_01318; -; 1.
 DR InterPro; IPR002143; Ribosomal_L1.
 DR InterPro; IPR005878; Ribosomal_L1b/c.
 DR Pfam; PF00687; Ribosomal_L1; 1.
 DR ProDom; PD001314; Ribosomal_L1; 1.
 DR TIGRFAMs; TIGR01169; rplA_bact; 1.
 DR PROSITE; PS01199; RIBOSOMAL_L1; 1.
 KW Ribosomal protein; RNA-binding; rRNA-binding; Antibiotic;
 KW Complete proteome.
 SQ SEQUENCE 234 AA; 25361 MW; 14C77CFC1483A2A4 CRC64;

Query Match 62.5%; Score 5; DB 1; Length 234;
 Best Local Similarity 100.0%; Pred. No. 89;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VNLDA 6
 |||||
 Db 223 VNLDA 227

RESULT 33

RGS1_HUMAN

ID RGS1_HUMAN STANDARD; PRT; 235 AA.
 AC Q9NS28;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Regulator of G-protein signaling 18 (RGS18).
 GN RGS18 OR RGS13.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang W., Wan T., Yuan Z., He L., Cao X.;
 RT "A novel regulator of G-protein signaling.";
 RL Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Platelet;
 RA Gagnon A.W., Murray D.L., Leadley R.J. Jr.;
 RT "Cloning and characterization of a novel regulator of G-protein
 RT signaling in human platelets.";
 RL Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX PubMed=11042171;
 RA Park I.K., Klug C.A., Li K., Jerabek L., Li L., Nanamori M.,
 RA Neubig R.R., Hood L., Weissman I.L., Clarke M.F.;
 RT "Molecular cloning and characterization of a novel regulator of
 RT G-protein signaling from mouse hematopoietic stem cells.";
 RL J. Biol. Chem. 276:915-923(2001).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;

```

RX  MEDLINE=22388257; PubMed=12477932;
RA  Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA  Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA  Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA  Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA  Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA  Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA  Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA  Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA  Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA  Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA  Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA  Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA  Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA  Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA  Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA  Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA  Schnierch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT  "Generation and initial analysis of more than 15,000 full-length
RT  human and mouse cDNA sequences.";
RL  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC  -!- FUNCTION: INHIBITS SIGNAL TRANSDUCTION BY INCREASING THE GTPASE
CC  ACTIVITY OF G PROTEIN ALPHA SUBUNITS THEREBY DRIVING THEM INTO
CC  THEIR INACTIVE GDP-BOUND FORM. BINDS TO G(I)-ALPHA AND G(Q)-ALPHA
CC  (BY SIMILARITY).
CC  -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC  -!- TISSUE SPECIFICITY: Expressed in peripheral leukocytes, bone
CC  marrow, spleen and fetal liver.
CC  -!- SIMILARITY: Contains 1 RGS domain.
CC  -----
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CC  use by non-profit institutions as long as its content is in no way
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CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; AF076642; AAF80227.1; -.
DR  EMBL; AF268036; AAK58589.1; -.
DR  EMBL; BC020632; AAH20632.1; -.
DR  HSSP; P49799; 1AGR.
DR  Genew; HGNC:14261; RGS18.
DR  MIM; 607192; -.
DR  InterPro; IPR000342; Regl_Gprotein.
DR  Pfam; PF00615; RGS; 1.
DR  PRINTS; PR01301; RGSPROTEIN.
DR  ProDom; PD001580; Regl_Gprotein; 1.
DR  SMART; SM00315; RGS; 1.
DR  PROSITE; PS50132; RGS; 1.
KW  Signal transduction inhibitor.
FT  DOMAIN      86      202      RGS.
FT  CONFLICT    226      227      DV -> ML (IN REF. 3).
SQ  SEQUENCE    235 AA;  27582 MW;  973ABDE8EC7DE3D5 CRC64;

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Query Match          62.5%;  Score 5;  DB 1;  Length 235;
Best Local Similarity 100.0%;  Pred. No. 89;

```

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLD 5
 |||||
 Db 150 EVNLD 154

RESULT 34

NPD_RHOBA

ID NPD_RHOBA STANDARD; PRT; 239 AA.
 AC Q7UFQ9;
 DT 15-MAR-2004 (Rel. 43, Created)
 DT 15-MAR-2004 (Rel. 43, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE NAD-dependent deacetylase (EC 3.5.1.-) (Regulatory protein SIR2 homolog).
 GN NPDA OR RB8404.
 OS Rhodopirellula baltica.
 OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
 OC Planctomycetaceae; Pirellula.
 OX NCBI_TaxID=117;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1;
 RX MEDLINE=22735913; PubMed=12835416;
 RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
 RA Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
 RA Schlesner H., Amann R., Reinhardt R.;
 RT "Complete genome sequence of the marine planctomycete Pirellula sp.
 RT strain 1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
 CC -!- FUNCTION: Modulates the activities of several enzymes which are
 CC inactive in their acetylated form (By similarity).
 CC -!- CATALYTIC ACTIVITY: NAD(+) + an acetylprotein = nicotinamide + O-
 CC acetyl-ADP-ribose + a protein.
 CC -!- COFACTOR: NAD (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
 CC -!- SIMILARITY: Belongs to the sirtuin family.
 CC -----
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 CC -----
 DR EMBL; BX294147; CAD78623.1; -.
 DR HAMAP; MF_01121; -; 1.
 DR PROSITE; PS50305; SIRTUIN; 1.
 KW Hydrolase; NAD.
 FT DOMAIN 1 239 DEACETYLASE SIRTUIN-TYPE.
 FT DOMAIN 8 21 NAD BINDING (BY SIMILARITY).
 FT ACT_SITE 111 111 BY SIMILARITY.
 SQ SEQUENCE 239 AA; 26142 MW; CB3FE5A5D385DDEF CRC64;

Query Match 62.5%; Score 5; DB 1; Length 239;

Best Local Similarity 100.0%; Pred. No. 90;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLD 5
 |||||
Db 205 EVNLD 209

RESULT 35

Y514 METJA

ID Y514 METJA STANDARD; PRT; 250 AA.

AC Q57934;

DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Hypothetical polyferredoxin-like protein MJ0514.

GN MJ0514.

OS Methanococcus jannaschii.

OC Archaea; Euryarchaeota; Methanococci; Methanococcales;

OC Methanocaldococcaceae; Methanocaldococcus.

OX NCBI_TaxID=2190;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;

RX MEDLINE=96337999; PubMed=8688087;

RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

RA Klerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
jannaschii.";

RL Science 273:1058-1073(1996).

CC -!- SIMILARITY: Belongs to the bacterial-type ferredoxin family.

CC

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CC

DR EMBL; U67501; AAB98503.1; -.

DR PIR; B64364; B64364.

DR HSSP; P00195; 1CLF.

DR TIGR; MJ0514; -.

DR InterPro; IPR001450; 4Fe4S_ferredoxin.

DR InterPro; IPR000813; 7Fe_ferredoxin.

DR Pfam; PF00037; fer4; 6.

DR PRINTS; PR00354; 7FE8SFRDOXIN.

DR PROSITE; PS00198; 4FE4S_FERREDOXIN; 6.

KW Hypothetical protein; Electron transport; Iron-sulfur; 4Fe-4S;

KW Repeat; Complete proteome.

FT	METAL	47	47	IRON-SULFUR (4FE-4S) (POTENTIAL).
FT	METAL	50	50	IRON-SULFUR (4FE-4S) (POTENTIAL).
FT	METAL	53	53	IRON-SULFUR (4FE-4S) (POTENTIAL).
FT	METAL	57	57	IRON-SULFUR (4FE-4S) (POTENTIAL).
FT	METAL	78	78	IRON-SULFUR (4FE-4S) (POTENTIAL).
FT	METAL	81	81	IRON-SULFUR (4FE-4S) (POTENTIAL).
FT	METAL	84	84	IRON-SULFUR (4FE-4S) (POTENTIAL).
FT	METAL	88	88	IRON-SULFUR (4FE-4S) (POTENTIAL).
FT	METAL	133	133	IRON-SULFUR (4FE-4S) (POTENTIAL).
FT	METAL	136	136	IRON-SULFUR (4FE-4S) (POTENTIAL).
FT	METAL	139	139	IRON-SULFUR (4FE-4S) (POTENTIAL).
FT	METAL	143	143	IRON-SULFUR (4FE-4S) (POTENTIAL).
FT	METAL	163	163	IRON-SULFUR (4FE-4S) (POTENTIAL).
FT	METAL	166	166	IRON-SULFUR (4FE-4S) (POTENTIAL).
FT	METAL	169	169	IRON-SULFUR (4FE-4S) (POTENTIAL).
FT	METAL	173	173	IRON-SULFUR (4FE-4S) (POTENTIAL).
FT	METAL	200	200	IRON-SULFUR (4FE-4S) (POTENTIAL).
FT	METAL	203	203	IRON-SULFUR (4FE-4S) (POTENTIAL).
FT	METAL	206	206	IRON-SULFUR (4FE-4S) (POTENTIAL).
FT	METAL	210	210	IRON-SULFUR (4FE-4S) (POTENTIAL).
FT	METAL	229	229	IRON-SULFUR (4FE-4S) (POTENTIAL).
FT	METAL	232	232	IRON-SULFUR (4FE-4S) (POTENTIAL).
FT	METAL	235	235	IRON-SULFUR (4FE-4S) (POTENTIAL).
FT	METAL	239	239	IRON-SULFUR (4FE-4S) (POTENTIAL).
SQ	SEQUENCE	250 AA; 28245 MW; 5C4D611D53ED2960 CRC64;		

Query Match 62.5%; Score 5; DB 1; Length 250;

Best Local Similarity 100.0%; Pred. No. 94;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLD 5
 |||||
 Db 157 EVNLD 161

RESULT 36

E1A_ADE41

ID E1A_ADE41 STANDARD; PRT; 251 AA.
 AC P10542;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Early E1A 27 kDa protein [Contains: Early E1A 25 kDa protein].
 OS Human adenovirus type 41.
 OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
 OX NCBI_TaxID=10524;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88084437; PubMed=2961652;
 RA van Loon A.E., Ligtenberg M., Reemst A.M.C.B., Sussenbach J.S.,
 RA Rozijn T.H.;
 RT "Structure and organization of the left-terminal DNA regions of
 RT fastidious adenovirus types 40 and 41."
 RL Gene 58:109-126(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88206069; PubMed=2834871;

RA Allard A., Wadell G.;
 RT "Physical organization of the enteric adenovirus type 41 early region
 RT 1A.";
 RL Virology 164:220-229(1988).
 CC -!- FUNCTION: Trans-activates early viral promoters and some cellular
 CC promoters.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Comment=Isoforms are derived from the E1 region of the genome;
 CC Name=1; Synonyms=Early E1A 27 kDa protein;
 CC IsoId=P10542-1; Sequence=Displayed;
 CC Name=2; Synonyms=Early E1A 25 kDa protein;
 CC IsoId=P10542-2; Sequence=VSP_000206;
 CC -----
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 CC -----
 DR EMBL; M18289; AAA42450.1; -.
 DR EMBL; M20300; AAA42439.1; -.
 DR EMBL; M20300; AAA42440.1; -.
 DR PIR; D27333; WMADF4.
 DR InterPro; IPR003853; Adeno_E1A.
 DR Pfam; PF02703; Adeno_E1A; 1.
 KW Transcription regulation; Activator; Early protein;
 KW Alternative splicing; Zinc-finger; DNA-binding.
 FT ZN_FING 150 170 C4-TYPE.
 FT VARSPLIC 154 181 Missing (in isoform 2).
 FT /FTId=VSP_000206.
 SQ SEQUENCE 251 AA; 27476 MW; BA48F87487EECE0B CRC64;

Query Match 62.5%; Score 5; DB 1; Length 251;
 Best Local Similarity 100.0%; Pred. No. 94;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVNLD 5
 |||||
 Db 92 EVNLD 96

RESULT 37

HEMK_BUCBP

ID HEMK_BUCBP STANDARD; PRT; 277 AA.
 AC Q89AT0;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE HemK protein homolog (EC 2.1.1.-).
 GN HEMK OR BBP162.
 OS Buchnera aphidicola (subsp. Baizongia pistaciae).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Buchnera.
 OX NCBI_TaxID=135842;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426901; PubMed=12522265;
 RA Van Ham R.C.H.J., Kamerbeek J., Palacios C., Rausell C., Abascal F.,
 RA Bastolla U., Fernandez J.M., Jimenez L., Postigo M., Silva F.J.,
 RA Tamames J., Viguera E., Latorre A., Valencia A., Moran F., Moya A.;
 RT "Reductive genome evolution in Buchnera aphidicola.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:581-586(2003).
 CC -!- SIMILARITY: Belongs to the hemK family.
 CC -----
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 CC -----
 DR EMBL; AE014016; AAO26895.1; -.
 DR InterPro; IPR002052; N6_Mtase.
 DR InterPro; IPR000051; SAM_bind.
 DR PROSITE; PS00092; N6_MTASE; UNKNOWN_1.
 KW Transferase; Methyltransferase; Complete proteome.
 SQ SEQUENCE 277 AA; 31965 MW; 80EC64C953975B3F CRC64;

Query Match 62.5%; Score 5; DB 1; Length 277;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 NLDAE 7
 |||||
 Db 22 NLDAE 26

RESULT 38

KPRS_METAC

ID KPRS_METAC STANDARD; PRT; 283 AA.
 AC Q8TRK8;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Ribose-phosphate pyrophosphokinase (EC 2.7.6.1) (RPPK) (Phosphoribosyl
 DE pyrophosphate synthetase) (P-Rib-PP synthetase) (PRPP synthetase).
 GN PRS OR MA1167.
 OS Methanosarcina acetivorans.
 OC Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
 OC Methanosarcinaceae; Methanosarcina.
 OX NCBI_TaxID=2214;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C2A / ATCC 35395 / DSM 2834;
 RX MEDLINE=21929760; PubMed=11932238;
 RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
 RA FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,
 RA Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,
 RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
 RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,

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RA Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,
RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,
RA Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,
RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
RA Metcalf W.W., Birren B.;
RT "The genome of Methanosarcina acetivorans reveals extensive metabolic
RT and physiological diversity.";
RL Genome Res. 12:532-542(2002).
CC -!- CATALYTIC ACTIVITY: ATP + D-ribose 5-phosphate = AMP + 5-phospho-
CC alpha-D-ribose 1-diphosphate.
CC -!- COFACTOR: Binds 1 magnesium ion per subunit (By similarity).
CC -!- PATHWAY: Utilized by both the de novo and the salvage pathways by
CC which endogenously formed or exogenously added pyrimidine, purine,
CC or pyridine bases are converted to the corresponding
CC ribonucleoside monophosphates.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the ribose-phosphate pyrophosphokinase
CC family.
CC -----
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CC -----
DR EMBL; AE010783; AAM04588.1; -.
DR HAMAP; MF_00583; -; 1.
DR InterPro; IPR000842; PRPP_synthetase.
DR InterPro; IPR000836; PRTransferase.
DR InterPro; IPR005946; RibP_Ppkin.
DR Pfam; PF00156; Pribosyltran; 1.
DR TIGRFAMs; TIGR01251; ribP_PPkin; 1.
DR PROSITE; PS00114; PRPP_SYNTHETASE; FALSE_NEG.
KW Nucleotide biosynthesis; Transferase; Kinase; Magnesium;
KW Complete proteome.
FT DOMAIN 201 214 BINDING OF PHOSPHORIBOSYLPYROPHOSPHATE
FT (POTENTIAL).
FT METAL 118 118 MAGNESIUM (POTENTIAL).
FT METAL 120 120 MAGNESIUM (POTENTIAL).
SQ SEQUENCE 283 AA; 30384 MW; 848CB5D1C257237F CRC64;

Query Match 62.5%; Score 5; DB 1; Length 283;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VNLDA 6
| | | |
Db 133 VNLDA 137

RESULT 39
G3P_LACDT
ID G3P_LACDT STANDARD; PRT; 290 AA.
AC P55070;

```

DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Glyceraldehyde 3-phosphate dehydrogenase (EC 1.2.1.12) (GAPDH)
 DE (Fragment).
 GN GPD.
 OS Lactarius deterrimus.
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
 OC Agaricales; Russulaceae; Lactarius.
 OX NCBI_TaxID=36060;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96387764; PubMed=8795234;
 RA Kreuzinger N., Podeu R., Gruber F., Gobl F., Kubicek C.P.;
 RT "Identification of some ectomycorrhizal basidiomycetes by PCR
 RT amplification of their gpd (glyceraldehyde-3-phosphate dehydrogenase)
 RT genes.";
 RL Appl. Environ. Microbiol. 62:3432-3438(1996).
 CC -!- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate + phosphate +
 CC NAD(+) = 3-phospho-D-glyceroyl phosphate + NADH.
 CC -!- PATHWAY: Second phase of glycolysis; first step.
 CC -!- SUBUNIT: Homotetramer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: Belongs to the glyceraldehyde 3-phosphate
 CC dehydrogenase family.

CC -----
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 CC -----

DR EMBL; U30876; AAB38369.1; -.
 DR HSSP; P00354; 3GPD.
 DR InterPro; IPR000173; GAP_dhdrogenase.
 DR Pfam; PF00044; gpdh; 1.
 DR Pfam; PF02800; gpdh_C; 1.
 DR PRINTS; PR00078; G3PDHDRGNASE.
 DR PROSITE; PS00071; GAPDH; 1.
 KW Glycolysis; Oxidoreductase; NAD.
 FT NON_TER 1 1
 FT BINDING 130 130 GLYCERALDEHYDE 3-PHOSPHATE.
 FT ACT_SITE 157 157 ACTIVATES THIOL GROUP DURING CATALYSIS.
 FT NON_TER 290 290
 SQ SEQUENCE 290 AA; 30768 MW; 4C2E77FAFDBF07CC CRC64;

Query Match 62.5%; Score 5; DB 1; Length 290;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VNLDA 6
 |||||
 Db 113 VNLDA 117

RESULT 40

G3P_BOLED

ID G3P_BOLED STANDARD; PRT; 291 AA.
AC Q00301;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Glyceraldehyde 3-phosphate dehydrogenase (EC 1.2.1.12) (GAPDH)
DE (Fragment).
GN GPD.
OS Boletus edulis (King bolete).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Boletales; Boletineae; Boletaceae; Boletus.
OX NCBI_TaxID=36056;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96387764; PubMed=8795234;
RA Kreuzinger N., Podeu R., Gruber F., Gobl F., Kubicek C.P.;
RT "Identification of some ectomycorrhizal basidiomycetes by PCR
RT amplification of their gpd (glyceraldehyde-3-phosphate dehydrogenase)
RT genes.";
RL Appl. Environ. Microbiol. 62:3432-3438(1996).
CC -!- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate + phosphate +
CC NAD(+) = 3-phospho-D-glyceroyl phosphate + NADH.
CC -!- PATHWAY: Second phase of glycolysis; first step.
CC -!- SUBUNIT: Homotetramer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the glyceraldehyde 3-phosphate
CC dehydrogenase family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U30625; AAB38246.1; -.
DR HSSP; P00357; 4GPD.
DR InterPro; IPR000173; GAP_dhydrogenase.
DR InterPro; IPR006424; GAPDH-I.
DR Pfam; PF00044; gpdh; 1.
DR Pfam; PF02800; gpdh_C; 1.
DR PRINTS; PR00078; G3PDHDRGNASE.
DR TIGRFAMs; TIGR01534; GAPDH-I; 1.
DR PROSITE; PS00071; GAPDH; 1.
KW Glycolysis; Oxidoreductase; NAD.
FT NON_TER 1 1
FT BINDING 130 130 GLYCERALDEHYDE 3-PHOSPHATE.
FT ACT_SITE 157 157 ACTIVATES THIOL GROUP DURING CATALYSIS.
FT NON_TER 291 291
SQ SEQUENCE 291 AA; 30895 MW; B497315405D6D287 CRC64;

Query Match 62.5%; Score 5; DB 1; Length 291;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VNLDA 6
 |||||
Db 113 VNLDA 117

Search completed: March 26, 2004, 15:33:43
Job time : 21.5 secs

924	4	50.0	166	4	US-08-723-142A-43	Sequence 43, Appl
925	4	50.0	166	4	US-09-528-784A-43	Sequence 43, Appl
926	4	50.0	166	4	US-09-499-148-1	Sequence 1, Appli
927	4	50.0	166	4	US-09-499-148-4	Sequence 4, Appli
928	4	50.0	166	4	US-09-252-991A-20150	Sequence 20150, A
929	4	50.0	166	4	US-09-569-098A-43	Sequence 43, Appl
930	4	50.0	166	4	US-08-529-055-48	Sequence 48, Appl
931	4	50.0	166	4	US-09-543-681A-5278	Sequence 5278, Ap
932	4	50.0	167	1	US-08-246-427A-2	Sequence 2, Appli
933	4	50.0	167	2	US-08-766-620-2	Sequence 2, Appli
934	4	50.0	167	4	US-08-858-207A-353	Sequence 353, App
935	4	50.0	167	4	US-09-318-786-31	Sequence 31, Appl
936	4	50.0	167	4	US-09-904-615-125	Sequence 125, App
937	4	50.0	167	5	PCT-US95-06094-2	Sequence 2, Appli
938	4	50.0	168	4	US-09-328-352-7986	Sequence 7986, Ap
939	4	50.0	168	4	US-08-529-055-55	Sequence 55, Appl
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943	4	50.0	170	4	US-09-489-039A-12433	Sequence 12433, A
944	4	50.0	171	1	US-08-438-753B-30	Sequence 30, Appl
945	4	50.0	171	1	US-08-443-883A-30	Sequence 30, Appl
946	4	50.0	171	2	US-08-631-328-30	Sequence 30, Appl
947	4	50.0	171	2	US-08-455-524B-30	Sequence 30, Appl
948	4	50.0	171	2	US-08-455-021B-30	Sequence 30, Appl
949	4	50.0	171	3	US-09-045-467-30	Sequence 30, Appl
950	4	50.0	171	4	US-09-107-532A-4012	Sequence 4012, Ap
951	4	50.0	172	1	US-08-438-753B-4	Sequence 4, Appli
952	4	50.0	172	1	US-08-438-753B-44	Sequence 44, Appl
953	4	50.0	172	1	US-08-443-883A-4	Sequence 4, Appli
954	4	50.0	172	1	US-08-443-883A-44	Sequence 44, Appl
955	4	50.0	172	2	US-08-631-328-4	Sequence 4, Appli
956	4	50.0	172	2	US-08-631-328-44	Sequence 44, Appl
957	4	50.0	172	2	US-08-455-524B-4	Sequence 4, Appli
958	4	50.0	172	2	US-08-455-524B-44	Sequence 44, Appl
959	4	50.0	172	2	US-08-455-021B-4	Sequence 4, Appli
960	4	50.0	172	2	US-08-455-021B-44	Sequence 44, Appl
961	4	50.0	172	3	US-08-149-101A-21	Sequence 21, Appl
962	4	50.0	172	3	US-09-045-467-4	Sequence 4, Appli
963	4	50.0	172	3	US-09-045-467-44	Sequence 44, Appl
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965	4	50.0	172	4	US-09-252-991A-18945	Sequence 18945, A
966	4	50.0	172	5	PCT-US94-12873-21	Sequence 21, Appl
967	4	50.0	173	3	US-08-923-454A-2	Sequence 2, Appli
968	4	50.0	174	3	US-08-149-101A-20	Sequence 20, Appl
969	4	50.0	174	4	US-09-198-452A-750	Sequence 750, App
970	4	50.0	174	4	US-09-785-669-2	Sequence 2, Appli
971	4	50.0	174	4	US-09-540-236-2201	Sequence 2201, Ap
972	4	50.0	174	5	PCT-US94-12873-20	Sequence 20, Appl
973	4	50.0	175	4	US-09-107-532A-6949	Sequence 6949, Ap
974	4	50.0	177	4	US-09-252-991A-28452	Sequence 28452, A
975	4	50.0	178	1	US-07-929-580B-2	Sequence 2, Appli
976	4	50.0	178	4	US-09-134-001C-2985	Sequence 2985, Ap
977	4	50.0	179	4	US-09-794-705A-7	Sequence 7, Appli
978	4	50.0	180	1	US-08-328-254-7	Sequence 7, Appli
979	4	50.0	180	2	US-08-624-650-1	Sequence 1, Appli
980	4	50.0	180	4	US-09-231-788-2	Sequence 2, Appli

981	4	50.0	180	4	US-09-818-648-1	Sequence 1, Appli
982	4	50.0	180	4	US-09-620-956-2	Sequence 2, Appli
983	4	50.0	180	4	US-09-620-956-12	Sequence 12, Appl
984	4	50.0	180	4	US-09-355-925-5	Sequence 5, Appli
985	4	50.0	180	4	US-09-611-152-2	Sequence 2, Appli
986	4	50.0	180	4	US-09-611-152-12	Sequence 12, Appl
987	4	50.0	180	4	US-09-252-991A-32768	Sequence 32768, A
988	4	50.0	180	4	US-09-480-297A-2	Sequence 2, Appli
989	4	50.0	180	4	US-09-480-297A-4	Sequence 4, Appli
990	4	50.0	180	4	US-09-794-705A-2	Sequence 2, Appli
991	4	50.0	180	4	US-09-747-259-2	Sequence 2, Appli
992	4	50.0	180	4	US-09-816-744-2	Sequence 2, Appli
993	4	50.0	180	4	US-09-787-375-2	Sequence 2, Appli
994	4	50.0	180	4	US-09-622-166A-3	Sequence 3, Appli
995	4	50.0	180	4	US-09-631-531-2	Sequence 2, Appli
996	4	50.0	180	4	US-09-631-531-12	Sequence 12, Appl
997	4	50.0	181	1	US-08-209-182C-4	Sequence 4, Appli
998	4	50.0	181	4	US-08-529-055-42	Sequence 42, Appl
999	4	50.0	181	4	US-09-486-147-5	Sequence 5, Appli
1000	4	50.0	181	4	US-09-540-236-3607	Sequence 3607, Ap

ALIGNMENTS

RESULT 1

US-08-802-981-219

; Sequence 219, Application US/08802981

; Patent No. 6037137

; GENERAL INFORMATION:

; APPLICANT: Komoriya, Akira

; APPLICANT: Packard, Beverly S.

; TITLE OF INVENTION: Compositions for the Detection of Enzyme

; TITLE OF INVENTION: Activity in Biological Samples and Methods of Use
Thereof

; NUMBER OF SEQUENCES: 231

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/802,981

; FILING DATE: 20-FEB-1997

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Hunter, Tom

; REGISTRATION NUMBER: 38,498

; REFERENCE/DOCKET NUMBER: 016865-000300US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 219:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-802-981-219

Query Match 100.0%; Score 8; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAEF 8
| | | | | | | |
Db 2 EVNLDAEF 9

RESULT 2

US-09-724-566A-52
; Sequence 52, Application US/09724566A
; Patent No. 6627739
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6627739mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEWC2
; CURRENT APPLICATION NUMBER: US/09/724,566A
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligopeptide substrate
US-09-724-566A-52

Query Match 100.0%; Score 8; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAEF 8
| | | | | | | |
Db 2 EVNLDAEF 9

RESULT 3

US-09-724-566A-83
; Sequence 83, Application US/09724566A
; Patent No. 6627739
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6627739mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEWC2
; CURRENT APPLICATION NUMBER: US/09/724,566A
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: APP fragment P5-P4'wt
US-09-724-566A-83

Query Match 100.0%; Score 8; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAEF 8
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Db 2 EVNLDAEF 9

RESULT 4

US-08-659-984A-19

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; Sequence 19, Application US/08659984A
; Patent No. 5942400
; GENERAL INFORMATION:
;   APPLICANT: Anderson, John P.
;   APPLICANT: Sinha, Sukanto
;   APPLICANT: Jacobson-Croak, Kirsten L.
;   TITLE OF INVENTION: Assays for Detecting Beta-Secretase
;   TITLE OF INVENTION: Inhibition
;   NUMBER OF SEQUENCES: 21
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Townsend and Townsend and Crew LLP
;     STREET: Two Embarcadero Ctr., 8th Floor
;     CITY: San Francisco
;     STATE: California
;     COUNTRY: USA
;     ZIP: 94111-3834
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/659,984A
;     FILING DATE: 07-JUN-1996
;     CLASSIFICATION: 436
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 08/485,152
;     FILING DATE: 07-JUN-1995
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Heslin, James M.
;     REGISTRATION NUMBER: 29,541
;     REFERENCE/DOCKET NUMBER: 15270-002810US
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 415-326-2400
;     TELEFAX: 415-326-2422
;   INFORMATION FOR SEQ ID NO: 19:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 10 amino acids
;       TYPE: amino acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;     MOLECULE TYPE: peptide
;     FEATURE:
;       NAME/KEY: Region
;       LOCATION: one-of(1)
;     OTHER INFORMATION: /note= "N-terminal Ser is acetylated."
US-08-659-984A-19

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Query Match 100.0%; Score 8; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.004;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 EVNLD AEF 8
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Db      2 EVNLD AEF 9

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RESULT 5

US-08-660-531-19

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; Sequence 19, Application US/08660531
; Patent No. 6221645
; GENERAL INFORMATION:
;   APPLICANT: Chrysler, Susanna M.S.
;   APPLICANT: Sinha, Sukanto
;   APPLICANT: Keim, Pamela S.
;   APPLICANT: Anderson, John P.
;   TITLE OF INVENTION: Beta-Secretase
;   NUMBER OF SEQUENCES: 21
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Townsend and Townsend and Crew LLP
;     STREET: Two Embarcadero Ctr., 8th Floor
;     CITY: San Francisco
;     STATE: California
;     COUNTRY: USA
;     ZIP: 94111-3834
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/660,531
;     FILING DATE:
;     CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 08/480,498
;     FILING DATE: 07-JUN-1995
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Heslin, James M.
;     REGISTRATION NUMBER: 29,541
;     REFERENCE/DOCKET NUMBER: 15270-002210US
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 415-326-2400
;     TELEFAX: 415-326-2422
;   INFORMATION FOR SEQ ID NO: 19:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 10 amino acids
;       TYPE: amino acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;     MOLECULE TYPE: peptide
;     FEATURE:
;       NAME/KEY: Region
;       LOCATION: one-of(1)
;     OTHER INFORMATION: /note= "N-terminal Ser is acetylated."
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US-08-660-531-19

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Query Match          100.0%; Score 8; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.004;
Matches      8; Conservative    0; Mismatches    0; Indels    0; Gaps    0;
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Qy          1 EVNLDAEF 8
             |||||
Db          2 EVNLDAEF 9
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RESULT 6

US-09-548-372D-63

; Sequence 63, Application US/09548372D

; Patent No. 6420534

; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR
AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 29915/6280I

; CURRENT APPLICATION NUMBER: US/09/548,372D

; CURRENT FILING DATE: 2000-04-12

; PRIOR APPLICATION NUMBER: US 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 63

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: Synthetic peptide

US-09-548-372D-63

Query Match 100.0%; Score 8; DB 4; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.004;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAEF 8

|||||||

Db 2 EVNLDAEF 9

RESULT 7

US-09-548-367D-63

; Sequence 63, Application US/09548367D

; Patent No. 6440698

; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR
AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 29915/6280H

; CURRENT APPLICATION NUMBER: US/09/548,367D

; CURRENT FILING DATE: 2000-04-12

; PRIOR APPLICATION NUMBER: US 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-548-367D-63

Query Match 100.0%; Score 8; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.004;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVNLDAEF 8
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Db 2 EVNLDAEF 9

RESULT 8

US-09-551-853D-63

; Sequence 63, Application US/09551853D
; Patent No. 6500667
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR
AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280L
; CURRENT APPLICATION NUMBER: US/09/551,853D
; CURRENT FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-551-853D-63

Query Match 100.0%; Score 8; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.004;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAEF 8
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Db 2 EVNLDAEF 9

RESULT 9

US-09-604-608-5

; Sequence 5, Application US/09604608
; Patent No. 6545127
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Lin, Xinli
; APPLICANT: Koelsch, Gerald
; TITLE OF INVENTION: Catalytically Active Recombinant Memapsin and Methods
; TITLE OF INVENTION: of Use Thereof
; FILE REFERENCE: OMRF 179
; CURRENT APPLICATION NUMBER: US/09/604,608
; CURRENT FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/141,363
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: 60/168,060
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: 60/177,836
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/178,368
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/210,292
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-604-608-5

Query Match 100.0%; Score 8; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.004;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAEF 8
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Db 2 EVNLDAEF 9

RESULT 10

PCT-US94-07043A-3

; Sequence 3, Application PC/TUS9407043A
; GENERAL INFORMATION:
; APPLICANT: Tamburini, Paul P.; Benz, G nter; H bich,
; APPLICANT: Dieter; Dreyer, Robert N.; Koenig, Gerhard
; TITLE OF INVENTION: CATHEPSIN D IS AN AMYLOIDOGENIC
; TITLE OF INVENTION: PROTEASE IN ALZHEIMER S DISEASE
; NUMBER OF SEQUENCES: 11

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Miles Inc.
; STREET: 400 Morgan Lane
; CITY: West Haven
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06516
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 800 kb storage
; COMPUTER: Sharp PC 4600
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07043A
; FILING DATE: June 21, 1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/10889
; FILING DATE: November 12, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/995,660
; FILING DATE: December 16, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/880,914
; FILING DATE: May 11, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Pamela A. Simonton
; REGISTRATION NUMBER: 31,060
; REFERENCE/DOCKET NUMBER: MTI 224.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203) 937-2340
; TELEFAX: (203) 937-2795
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
PCT-US94-07043A-3

```

```

Query Match          100.0%; Score 8; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0044;
Matches      8; Conservative    0; Mismatches    0; Indels      0; Gaps      0;

```

```

Qy      1 EVNLDAEF 8
        |||||
Db      3 EVNLDAEF 10

```

```

RESULT 11
US-08-659-984A-18
; Sequence 18, Application US/08659984A
; Patent No. 5942400
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Jacobson-Croak, Kirsten L.
; TITLE OF INVENTION: Assays for Detecting Beta-Secretase

```



```

; TITLE OF INVENTION: Inhibition
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/659,984A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,152
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-002810US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-659-984A-18

```

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Query Match          100.0%; Score 8; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0081;
Matches      8; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

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```

Qy      1 EVNLDAEF 8
        |||||
Db      2 EVNLDAEF 9

```

```

RESULT 12
US-08-802-981-112
; Sequence 112, Application US/08802981
; Patent No. 6037137
; GENERAL INFORMATION:
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly S.
; TITLE OF INVENTION: Compositions for the Detection of Enzyme
; TITLE OF INVENTION: Activity in Biological Samples and Methods of Use
; Thereof
; NUMBER OF SEQUENCES: 231

```

```

;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  Townsend and Townsend and Crew LLP
;   STREET:    Two Embarcadero Center, Eighth Floor
;   CITY:      San Francisco
;   STATE:     California
;   COUNTRY:   USA
;   ZIP:       94111-3834
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE:  Floppy disk
;   COMPUTER:    IBM PC compatible
;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:    PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/802,981
;   FILING DATE:      20-FEB-1997
;   CLASSIFICATION:    435
;   ATTORNEY/AGENT INFORMATION:
;   NAME:             Hunter, Tom
;   REGISTRATION NUMBER:  38,498
;   REFERENCE/DOCKET NUMBER:  016865-000300US
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:        (415) 576-0200
;   TELEFAX:          (415) 576-0300
;   INFORMATION FOR SEQ ID NO:  112:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:           21 amino acids
;   TYPE:              amino acid
;   STRANDEDNESS:
;   TOPOLOGY:         linear
;   MOLECULE TYPE:     peptide
;   FEATURE:
;   NAME/KEY:          Modified-site
;   LOCATION:          3
;   OTHER INFORMATION:  /product= "Aib"
;   FEATURE:
;   NAME/KEY:          Modified-site
;   LOCATION:          4
;   OTHER INFORMATION:  /product= "Acp"
;   FEATURE:
;   NAME/KEY:          Modified-site
;   LOCATION:          16
;   OTHER INFORMATION:  /product= "Acp"
US-08-802-981-112

```

```

Query Match          100.0%;  Score 8;  DB 3;  Length 21;
Best Local Similarity 100.0%;  Pred. No. 0.0081;
Matches      8;  Conservative    0;  Mismatches    0;  Indels      0;  Gaps      0;

```

```

Qy          1 EVNLDAEF 8
            |||||
Db          7 EVNLDAEF 14

```

```

RESULT 13
US-08-660-531-18
; Sequence 18, Application US/08660531
; Patent No. 6221645

```

```

; GENERAL INFORMATION:
; APPLICANT: Chrysler, Susanna M.S.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Keim, Pamela S.
; APPLICANT: Anderson, John P.
; TITLE OF INVENTION: Beta-Secretase
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,531
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/480,498
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-002210US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-660-531-18

```

```

Query Match          100.0%; Score 8; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0081;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 EVNLDAEF 8
        |||||
Db      2 EVNLDAEF 9

```

```

RESULT 14
US-08-659-984A-17
; Sequence 17, Application US/08659984A
; Patent No. 5942400
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.

```

```

; APPLICANT: Sinha, Sukanto
; APPLICANT: Jacobson-Croak, Kirsten L.
; TITLE OF INVENTION: Assays for Detecting Beta-Secretase
; TITLE OF INVENTION: Inhibition
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/659,984A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,152
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-002810US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-659-984A-17

```

```

Query Match          100.0%; Score 8; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches      8; Conservative    0; Mismatches    0; Indels      0; Gaps      0;

```

```

Qy      1 EVNLDAEF 8
        |||||
Db      23 EVNLDAEF 30

```

```

RESULT 15
US-08-660-531-17
; Sequence 17, Application US/08660531
; Patent No. 6221645
; GENERAL INFORMATION:
; APPLICANT: Chrysler, Susanna M.S.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Keim, Pamela S.

```

```

; APPLICANT: Anderson, John P.
; TITLE OF INVENTION: Beta-Secretase
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,531
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/480,498
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-002210US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-660-531-17

```

```

Query Match          100.0%; Score 8; DB 3; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 EVNLDAEF 8
        |||||
Db      23 EVNLDAEF 30

```

```

RESULT 16
US-09-724-566A-53
; Sequence 53, Application US/09724566A
; Patent No. 6627739
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6627739mand
; APPLICANT: John, Varghese

```

```

; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEWC2
; CURRENT APPLICATION NUMBER: US/09/724,566A
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligopeptide substrate
US-09-724-566A-53

```

```

Query Match          100.0%; Score 8; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches      8; Conservative    0; Mismatches    0; Indels      0; Gaps      0;

```

```

Qy      1 EVNLDAEF 8
        |||||
Db      23 EVNLDAEF 30

```

RESULT 17

US-08-659-984A-16

```

; Sequence 16, Application US/08659984A
; Patent No. 5942400
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Jacobson-Croak, Kirsten L.
; TITLE OF INVENTION: Assays for Detecting Beta-Secretase
; TITLE OF INVENTION: Inhibition
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

```

```

;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/659,984A
;   FILING DATE:  07-JUN-1996
;   CLASSIFICATION:  436
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  US 08/485,152
;   FILING DATE:  07-JUN-1995
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  Heslin, James M.
;   REGISTRATION NUMBER:  29,541
;   REFERENCE/DOCKET NUMBER:  15270-002810US
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  415-326-2400
;   TELEFAX:  415-326-2422
;   INFORMATION FOR SEQ ID NO:  16:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  33 amino acids
;   TYPE:  amino acid
;   STRANDEDNESS:  single
;   TOPOLOGY:  linear
;   MOLECULE TYPE:  peptide
US-08-659-984A-16

```

```

Query Match          100.0%;  Score 8;  DB 2;  Length 33;
Best Local Similarity 100.0%;  Pred. No. 0.012;
Matches      8;  Conservative    0;  Mismatches    0;  Indels      0;  Gaps      0;

```

```

Qy      1 EVNLDAEF 8
        |||||
Db      14 EVNLDAEF 21

```

RESULT 18

US-08-660-531-16

```

; Sequence 16, Application US/08660531
; Patent No. 6221645
;   GENERAL INFORMATION:
;   APPLICANT:  Chrysler, Susanna M.S.
;   APPLICANT:  Sinha, Sukanto
;   APPLICANT:  Keim, Pamela S.
;   APPLICANT:  Anderson, John P.
;   TITLE OF INVENTION:  Beta-Secretase
;   NUMBER OF SEQUENCES:  21
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  Townsend and Townsend and Crew LLP
;   STREET:  Two Embarcadero Ctr., 8th Floor
;   CITY:  San Francisco
;   STATE:  California
;   COUNTRY:  USA
;   ZIP:  94111-3834
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE:  Floppy disk
;   COMPUTER:  IBM PC compatible
;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.25

```

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,531
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/480,498
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-002210US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-660-531-16

```

```

Query Match          100.0%; Score 8; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches      8; Conservative    0; Mismatches    0; Indels      0; Gaps      0;

```

```

Qy      1 EVNLDAEF 8
        |||||
Db      14 EVNLDAEF 21

```

RESULT 19

US-09-724-566A-63

```

; Sequence 63, Application US/09724566A
; Patent No. 6627739
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6627739mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEWC2
; CURRENT APPLICATION NUMBER: US/09/724,566A
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10

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; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 63
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: P26-P4'sw peptide substrate
US-09-724-566A-63

Query Match 100.0%; Score 8; DB 4; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAEF 8
| | | | | | | |
Db 26 EVNLDAEF 33

RESULT 20

US-08-659-984A-15

; Sequence 15, Application US/08659984A
; Patent No. 5942400
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Jacobson-Croak, Kirsten L.
; TITLE OF INVENTION: Assays for Detecting Beta-Secretase
; TITLE OF INVENTION: Inhibition
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/659,984A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,152
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-002810US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400

; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-659-984A-15

Query Match 100.0%; Score 8; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAEF 8
| | | | | | | |
Db 23 EVNLDAEF 30

RESULT 21

US-08-660-531-15

; Sequence 15, Application US/08660531
; Patent No. 6221645

; GENERAL INFORMATION:

; APPLICANT: Chrysler, Susanna M.S.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Keim, Pamela S.
; APPLICANT: Anderson, John P.

; TITLE OF INVENTION: Beta-Secretase

; NUMBER OF SEQUENCES: 21

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/660,531

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/480,498

; FILING DATE: 07-JUN-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Heslin, James M.

; REGISTRATION NUMBER: 29,541

; REFERENCE/DOCKET NUMBER: 15270-002210US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-326-2400

; TELEFAX: 415-326-2422

; INFORMATION FOR SEQ ID NO: 15:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-660-531-15

Query Match 100.0%; Score 8; DB 3; Length 42;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAEF 8
|||||||
Db 23 EVNLDAEF 30

RESULT 22

US-08-339-708A-12

; Sequence 12, Application US/08339708A
; Patent No. 6037521

; GENERAL INFORMATION:

; APPLICANT: Sato, Masahiro
; APPLICANT: Takashi, Kobayashi
; APPLICANT: Tada, No. 6037521hihiro
; APPLICANT: Shoji, Mikio
; APPLICANT: Kawarabayashi, Takeshi
; TITLE OF INVENTION: TRANSGENIC ANIMAL MODEL FOR ALZHEIMER'S
; TITLE OF INVENTION: DISEASE
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/339,708A
; FILING DATE: 14-NOV-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 306026/93
; FILING DATE: 12-NOV-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: SANDERCOCK, COLIN G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 026083/0159

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136

; INFORMATION FOR SEQ ID NO: 12:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 103 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-339-708A-12

Query Match 100.0%; Score 8; DB 3; Length 103;
Best Local Similarity 100.0%; Pred. No. 0.036;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAEF 8
|||
Db 1 EVNLDAEF 8

RESULT 23

US-08-659-984A-21
; Sequence 21, Application US/08659984A
; Patent No. 5942400
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Jacobson-Croak, Kirsten L.
; TITLE OF INVENTION: Assays for Detecting Beta-Secretase
; TITLE OF INVENTION: Inhibition
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/659,984A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,152
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-002810US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 506 amino acids
; TYPE: amino acid

; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-659-984A-21

Query Match 100.0%; Score 8; DB 2; Length 506;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAEF 8
| | | | | | | |
Db 404 EVNLDAEF 411

RESULT 24

US-08-660-531-21

; Sequence 21, Application US/08660531
; Patent No. 6221645

; GENERAL INFORMATION:

; APPLICANT: Chrysler, Susanna M.S.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Keim, Pamela S.
; APPLICANT: Anderson, John P.
; TITLE OF INVENTION: Beta-Secretase
; NUMBER OF SEQUENCES: 21

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/660,531
; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/480,498
; FILING DATE: 07-JUN-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-002210US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422

; INFORMATION FOR SEQ ID NO: 21:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 506 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-660-531-21

Query Match 100.0%; Score 8; DB 3; Length 506;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAEF 8
| | | | | | | |
Db 404 EVNLDAEF 411

RESULT 25

US-09-054-334-4

; Sequence 4, Application US/09054334
; Patent No. 6329163
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Jacobson-Croak, Kirsten L.
; APPLICANT: Sinha, Sukanto
; TITLE OF INVENTION: Assays for Detecting Beta-Secretase
; TITLE OF INVENTION: Inhibition
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcader Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/054,334
; FILING DATE: 02-APR-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,152
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 015270-002820US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 506 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-054-334-4

Query Match 100.0%; Score 8; DB 4; Length 506;
Best Local Similarity 100.0%; Pred. No. 0.16;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAEF 8
 |||||

Db 404 EVNLDAEF 411

RESULT 26

US-09-548-372D-12
 ; Sequence 12, Application US/09548372D
 ; Patent No. 6420534
 ; GENERAL INFORMATION:
 ; APPLICANT: GURNEY ET AL.
 ; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR
 AND USES
 ; TITLE OF INVENTION: THEREOF
 ; FILE REFERENCE: 29915/6280I
 ; CURRENT APPLICATION NUMBER: US/09/548,372D
 ; CURRENT FILING DATE: 2000-04-12
 ; PRIOR APPLICATION NUMBER: US 60/155,493
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: US 09/404,133
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: PCT/US99/20881
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: US 60/101,594
 ; PRIOR FILING DATE: 1998-09-24
 ; NUMBER OF SEQ ID NOS: 73
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 12
 ; LENGTH: 695
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-548-372D-12

Query Match 100.0%; Score 8; DB 4; Length 695;
 Best Local Similarity 100.0%; Pred. No. 0.21;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAEF 8
 |||||

Db 593 EVNLDAEF 600

RESULT 27

US-09-548-367D-12
 ; Sequence 12, Application US/09548367D
 ; Patent No. 6440698
 ; GENERAL INFORMATION:
 ; APPLICANT: GURNEY ET AL.
 ; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR
 AND USES
 ; TITLE OF INVENTION: THEREOF
 ; FILE REFERENCE: 29915/6280H
 ; CURRENT APPLICATION NUMBER: US/09/548,367D
 ; CURRENT FILING DATE: 2000-04-12
 ; PRIOR APPLICATION NUMBER: US 60/155,493

; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 695
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-367D-12

Query Match 100.0%; Score 8; DB 4; Length 695;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLD AEF 8
| | | | |
Db 593 EVNLD AEF 600

RESULT 28

US-09-551-853D-12
; Sequence 12, Application US/09551853D
; Patent No. 6500667
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR
AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280L
; CURRENT APPLICATION NUMBER: US/09/551,853D
; CURRENT FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 695
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-551-853D-12

Query Match 100.0%; Score 8; DB 4; Length 695;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLD AEF 8

Db |||||
593 EVNLDAEF 600

RESULT 29

US-09-548-372D-18
; Sequence 18, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR
AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280I
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-372D-18

Query Match 100.0%; Score 8; DB 4; Length 697;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAEF 8
 |||||
Db 593 EVNLDAEF 600

RESULT 30

US-09-548-367D-18
; Sequence 18, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR
AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-367D-18

Query Match 100.0%; Score 8; DB 4; Length 697;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAEF 8
| | | | | | | |
Db 593 EVNLDAEF 600

RESULT 31

US-09-551-853D-18
; Sequence 18, Application US/09551853D
; Patent No. 6500667
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR
AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280L
; CURRENT APPLICATION NUMBER: US/09/551,853D
; CURRENT FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-551-853D-18

Query Match 100.0%; Score 8; DB 4; Length 697;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAEF 8
| | | | | | | |
Db 593 EVNLDAEF 600

RESULT 32

US-09-252-991A-24809

; Sequence 24809, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 24809
 ; LENGTH: 371
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-24809

Query Match 75.0%; Score 6; DB 4; Length 371;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDA 6
 |||||
 Db 184 EVNLDA 189

RESULT 33

US-08-480-498-2

; Sequence 2, Application US/08480498
 ; Patent No. 5744346
 ; GENERAL INFORMATION:
 ; APPLICANT: Chrysler, Susanna M.S.
 ; APPLICANT: Sinha, Sukanto
 ; APPLICANT: Keim, Pamela S.
 ; APPLICANT: Anderson, John P.
 ; TITLE OF INVENTION: Beta-Secretase
 ; NUMBER OF SEQUENCES: 3
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend Khourie and Crew
 ; STREET: One Market Plaza, Steuart Tower, Suite 2000
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94105
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/480,498
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 015270-002200
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-480-498-2

Query Match 62.5%; Score 5; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VNLDA 6
|||||
Db 1 VNLDA 5

RESULT 34

US-08-659-984A-14

; Sequence 14, Application US/08659984A
; Patent No. 5942400
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Jacobson-Croak, Kirsten L.
; TITLE OF INVENTION: Assays for Detecting Beta-Secretase
; TITLE OF INVENTION: Inhibition
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/659,984A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,152

```

; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-002810US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-659-984A-14

```

```

Query Match          62.5%; Score 5; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches      5; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      2 VNLDA 6
        |||||
Db      1 VNLDA 5

```

RESULT 35

US-08-660-531-14

```

; Sequence 14, Application US/08660531
; Patent No. 6221645
; GENERAL INFORMATION:
; APPLICANT: Chrysler, Susanna M.S.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Keim, Pamela S.
; APPLICANT: Anderson, John P.
; TITLE OF INVENTION: Beta-Secretase
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,531
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/480,498
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:

```

; NAME: Heslin, James M.
 ; REGISTRATION NUMBER: 29,541
 ; REFERENCE/DOCKET NUMBER: 15270-002210US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-326-2400
 ; TELEFAX: 415-326-2422
 ; INFORMATION FOR SEQ ID NO: 14:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 US-08-660-531-14

Query Match 62.5%; Score 5; DB 3; Length 5;
 Best Local Similarity 100.0%; Pred. No. 3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VNLDA 6
 |||||
 Db 1 VNLDA 5

RESULT 36

US-09-054-334-2

; Sequence 2, Application US/09054334
 ; Patent No. 6329163
 ; GENERAL INFORMATION:
 ; APPLICANT: Anderson, John P.
 ; APPLICANT: Jacobson-Croak, Kirsten L.
 ; APPLICANT: Sinha, Sukanto
 ; TITLE OF INVENTION: Assays for Detecting Beta-Secretase
 ; TITLE OF INVENTION: Inhibition
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcader Center, Eighth Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-3834
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/054,334
 ; FILING DATE: 02-APR-1998
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/485,152
 ; FILING DATE: 07-JUN-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Heslin, James M.
 ; REGISTRATION NUMBER: 29,541

; REFERENCE/DOCKET NUMBER: 015270-002820US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-054-334-2

Query Match 62.5%; Score 5; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VNLDA 6
|||||
Db 1 VNLDA 5

RESULT 37

US-09-724-566A-51

; Sequence 51, Application US/09724566A
; Patent No. 6627739
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6627739mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEWC2
; CURRENT APPLICATION NUMBER: US/09/724,566A
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-566A-51

Query Match 62.5%; Score 5; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VNLDA 6
|||||
Db 1 VNLDA 5

RESULT 38

US-08-136-743B-33

; Sequence 33, Application US/08136743B

; Patent No. 5459063

; GENERAL INFORMATION:

; APPLICANT: Barry S. Cooperman, Harvey Rubin,

; APPLICANT: Jerome Salem, and Alison L. Fisher

; TITLE OF INVENTION: "Plasmodium falciparum Ribonu-

; TITLE OF INVENTION: cleotide Reductase, DNA Sequences Therefor and Peptide
inhibitor

; TITLE OF INVENTION: Thereof"

; NUMBER OF SEQUENCES: 67

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: The University of Pennsylvania

; STREET: Suite 330

; STREET: 3700 Market Street

; CITY: Philadelphia

; STATE: Pennsylvania

; COUNTRY: U.S.A.

; ZIP: 19104-3246

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb

; COMPUTER: IBM PS/2

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: WordPerfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/136,743B

; FILING DATE: 10/14/93

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Monaco, Daniel A.

; REGISTRATION NUMBER: 30,480

; REFERENCE/DOCKET NUMBER: 3957-10

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (215) 568-8383

; TELEFAX: (215) 568-5549

; TELEX: No. 5459063e

; INFORMATION FOR SEQ ID NO: 33:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 7 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

US-08-136-743B-33

Query Match 62.5%; Score 5; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LDAEF 8
|||||
Db 3 LDAEF 7

RESULT 39

US-08-136-743B-35

; Sequence 35, Application US/08136743B

; Patent No. 5459063

; GENERAL INFORMATION:

; APPLICANT: Barry S. Cooperman, Harvey Rubin,

; APPLICANT: Jerome Salem, and Alison L. Fisher

; TITLE OF INVENTION: "Plasmodium falciparum Ribonu-

; TITLE OF INVENTION: cleotide Reductase, DNA Sequences Therefor and Peptide inhibitor

; TITLE OF INVENTION: Thereof"

; NUMBER OF SEQUENCES: 67

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: The University of Pennsylvania

; STREET: Suite 330

; STREET: 3700 Market Street

; CITY: Philadelphia

; STATE: Pennsylvania

; COUNTRY: U.S.A.

; ZIP: 19104-3246

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb

; COMPUTER: IBM PS/2

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: WordPerfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/136,743B

; FILING DATE: 10/14/93

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Monaco, Daniel A.

; REGISTRATION NUMBER: 30,480

; REFERENCE/DOCKET NUMBER: 3957-10

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (215) 568-8383

; TELEFAX: (215) 568-5549

; TELEX: No. 5459063e

; INFORMATION FOR SEQ ID NO: 35:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 7 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

US-08-136-743B-35

Query Match 62.5%; Score 5; DB 1; Length 7;

Best Local Similarity 100.0%; Pred. No. 3e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LDAEF 8
|||||
Db 3 LDAEF 7

RESULT 40
 US-08-136-743B-56
 ; Sequence 56, Application US/08136743B
 ; Patent No. 5459063
 ; GENERAL INFORMATION:
 ; APPLICANT: Barry S. Cooperman, Harvey Rubin,
 ; APPLICANT: Jerome Salem, and Alison L. Fisher
 ; TITLE OF INVENTION: "Plasmodium falciparum Ribonu-
 ; TITLE OF INVENTION: cleotide Reductase, DNA Sequences Therefor and Peptide
 inhibitor
 ; TITLE OF INVENTION: Thereof"
 ; NUMBER OF SEQUENCES: 67
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: The University of Pennsylvania
 ; STREET: Suite 330
 ; STREET: 3700 Market Street
 ; CITY: Philadelphia
 ; STATE: Pennsylvania
 ; COUNTRY: U.S.A.
 ; ZIP: 19104-3246
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
 ; COMPUTER: IBM PS/2
 ; OPERATING SYSTEM: MS-DOS
 ; SOFTWARE: WordPerfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/136,743B
 ; FILING DATE: 10/14/93
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Monaco, Daniel A.
 ; REGISTRATION NUMBER: 30,480
 ; REFERENCE/DOCKET NUMBER: 3957-10
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (215) 568-8383
 ; TELEFAX: (215) 568-5549
 ; TELEX: No. 5459063e
 ; INFORMATION FOR SEQ ID NO: 56:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 7 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 US-08-136-743B-56

Query Match 62.5%; Score 5; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 4 LDAEF 8
 |||||
 Db 3 LDAEF 7

Search completed: March 26, 2004, 15:36:16
 Job time : 24.5 secs

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OM protein - protein search, using sw model

Run on: March 26, 2004, 15:30:37 ; Search time 13.5 Seconds
(without alignments)
57.002 Million cell updates/sec

Title: US-09-668-314C-71
Perfect score: 8
Sequence: 1 EVNLDAEF 8

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283366 seqs, 96191526 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : PIR_78:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	7	87.5	419	2	D42725		nitrile hydratase
2	6	75.0	295	2	F83867		dihydrodipicolinat
3	6	75.0	326	2	A83087		conserved hypothet
4	6	75.0	368	2	A28825		keratin, type I no
5	6	75.0	394	2	F69888		alanine racemase h
6	6	75.0	619	1	JH0776		hydrogenase (EC 1.
7	6	75.0	802	2	C90326		hypothetical prote
8	6	75.0	868	2	G82193		aminopeptidase N V
9	6	75.0	4639	1	A54794		dynein heavy chain
10	5	62.5	73	2	S40015		phd protein - phag
11	5	62.5	91	2	S57268		translation elonga
12	5	62.5	91	2	A75188		translation elonga
13	5	62.5	105	2	T37632		hypothetical prote

14	5	62.5	110	2	S65003	hypothetical prote
15	5	62.5	119	2	F83714	holo-(acyl carrier
16	5	62.5	126	2	T18655	hypothetical prote
17	5	62.5	126	2	AH1425	hypothetical secre
18	5	62.5	135	2	H69419	arsenate reductase
19	5	62.5	136	2	H72633	hypothetical prote
20	5	62.5	142	2	S77399	urease accessory p
21	5	62.5	144	2	B83069	hypothetical prote
22	5	62.5	147	2	S75581	hypothetical prote
23	5	62.5	148	2	AH1166	ribose 5-phosphate
24	5	62.5	151	2	AC0407	ribose-5-phosphate
25	5	62.5	166	2	B70800	hypothetical prote
26	5	62.5	168	2	G82898	conserved hypothet
27	5	62.5	170	2	T08348	hypothetical prote
28	5	62.5	172	2	F65038	hypothetical prote
29	5	62.5	172	2	B91062	hypothetical prote
30	5	62.5	172	2	F85906	hypothetical prote
31	5	62.5	172	2	H81251	NADH2 dehydrogenas
32	5	62.5	173	2	S67579	probable membrane
33	5	62.5	182	2	E64678	NADH2 dehydrogenas
34	5	62.5	182	2	C71839	NADH2 dehydrogenas
35	5	62.5	184	2	AE2330	adenylate kinase [
36	5	62.5	197	2	S61047	hypothetical prote
37	5	62.5	197	2	E64102	skp protein - Haem
38	5	62.5	200	2	AG0986	hypothetical luxR-
39	5	62.5	202	2	A53646	rho GDP dissociati
40	5	62.5	205	2	S78221	G-protein signalin
41	5	62.5	208	2	F95892	probable glutathio
42	5	62.5	212	2	E75334	ribonuclease HII -
43	5	62.5	214	2	A87276	hypothetical prote
44	5	62.5	217	1	I67685	nitroreductase (EC
45	5	62.5	217	1	S08397	nitroreductase (EC
46	5	62.5	217	2	H90705	oxygen-insensitive
47	5	62.5	217	2	C85556	oxygen-insensitive
48	5	62.5	217	2	AD0573	oxygen-insensitive
49	5	62.5	222	2	G83125	conserved hypothet
50	5	62.5	228	2	A96918	probable enzyme wi
51	5	62.5	229	2	D71362	hypothetical prote
52	5	62.5	231	2	A87625	cell cycle transcr
53	5	62.5	232	2	AI3304	response regulator
54	5	62.5	233	2	T03329	probable amidase 1
55	5	62.5	234	2	E71846	ribosomal protein
56	5	62.5	234	2	A97652	response regulator
57	5	62.5	234	2	AH2875	two component resp
58	5	62.5	237	2	H90492	ABC transporter, A
59	5	62.5	240	2	E82331	conserved hypothet
60	5	62.5	246	2	AI2990	3-oxoacyl-(acyl-ca
61	5	62.5	246	2	H98292	3-oxoacyl-(acyl-ca
62	5	62.5	250	2	B64364	polyferredoxin 1 -
63	5	62.5	251	1	WMADF4	early E1A 27K prot
64	5	62.5	254	2	AE2516	hypothetical prote
65	5	62.5	259	2	T51745	RNA helicase RH16
66	5	62.5	264	2	AG3466	transcription regu
67	5	62.5	278	2	A72411	hypothetical prote
68	5	62.5	280	2	T09939	hypothetical prote
69	5	62.5	282	2	T26112	hypothetical prote
70	5	62.5	289	2	T40596	probable DNA repai

71	5	62.5	292	2	D95282	probable LysR type
72	5	62.5	292	2	G97347	acetyltransferase
73	5	62.5	305	2	S32237	hypothetical prote
74	5	62.5	308	2	C90424	cyclase/dehydrase,
75	5	62.5	313	2	D75403	hypothetical prote
76	5	62.5	321	2	A82070	transcription regu
77	5	62.5	324	2	I39563	probable UDPglucos
78	5	62.5	326	2	T11721	conserved hypothet
79	5	62.5	330	1	QQBEP7	gene 62 protein -
80	5	62.5	330	2	T42975	hypothetical prote
81	5	62.5	332	2	A22366	glyceraldehyde-3-p
82	5	62.5	332	2	B22366	glyceraldehyde-3-p
83	5	62.5	332	2	S24630	glyceraldehyde-3-p
84	5	62.5	334	2	S51570	hypothetical prote
85	5	62.5	337	1	DEUSGM	glyceraldehyde-3-p
86	5	62.5	337	2	S26974	glyceraldehyde-3-p
87	5	62.5	341	2	T22746	hypothetical prote
88	5	62.5	343	2	AB1086	ATP synthase delta
89	5	62.5	344	2	S38939	probable cathepsin
90	5	62.5	344	2	F81911	probable phosphori
91	5	62.5	344	2	E81104	phosphoribosylform
92	5	62.5	346	2	D75356	anthranilate synth
93	5	62.5	348	2	B83869	hypothetical prote
94	5	62.5	350	2	C87084	phenylalanyl-tRNA
95	5	62.5	350	2	E64499	hypothetical prote
96	5	62.5	350	2	B75192	hypothetical prote
97	5	62.5	350	2	E75341	peptidyl-prolyl ci
98	5	62.5	351	2	B49906	rfbB homolog - Xan
99	5	62.5	354	2	AF1037	probable major cap
100	5	62.5	357	2	AI2937	hypothetical prote
101	5	62.5	357	2	AI2938	hypothetical prote
102	5	62.5	357	2	F98344	lactose transport
103	5	62.5	357	2	H84240	integrase/recombin
104	5	62.5	358	2	E95842	probable lactose t
105	5	62.5	358	2	T29744	hypothetical prote
106	5	62.5	359	2	T08815	choline kinase (EC
107	5	62.5	359	2	AF3044	hypothetical prote
108	5	62.5	360	1	S30109	D-vitopine dehydro
109	5	62.5	361	2	F96034	probable sugar upt
110	5	62.5	361	2	AF2943	hypothetical prote
111	5	62.5	361	2	D98339	lactose transport
112	5	62.5	362	2	E95972	probable sugar upt
113	5	62.5	363	2	S34734	ATP-binding protei
114	5	62.5	366	2	E64334	2-oxoacid-ferredox
115	5	62.5	366	2	AE0105	sugar transport AT
116	5	62.5	367	2	F98343	mtlK protein (AF00
117	5	62.5	370	2	S77011	mercuric resistanc
118	5	62.5	371	1	A43830	alanine dehydrogen
119	5	62.5	371	2	F87100	L-alanine dehydrog
120	5	62.5	371	2	AH3169	hypothetical prote
121	5	62.5	374	2	F98241	mtlK protein (AF00
122	5	62.5	375	2	C75452	translation releas
123	5	62.5	378	2	T30435	very late factor 1
124	5	62.5	380	2	AC3360	nitrogen regulatio
125	5	62.5	380	2	T42755	tyrosylprotein sul
126	5	62.5	383	2	T23057	hypothetical prote
127	5	62.5	384	2	D87471	ROK family protein

128	5	62.5	384	2	T08318	conserved hypothet
129	5	62.5	390	1	S58814	cell division prot
130	5	62.5	391	2	T20752	hypothetical prote
131	5	62.5	395	2	G75046	pyruvate synthase
132	5	62.5	396	2	T45088	pyruvate synthase
133	5	62.5	397	2	S70987	dnaN protein - Myc
134	5	62.5	398	2	E71114	probable ferredoxi
135	5	62.5	398	2	C95201	hydroxymethylgluta
136	5	62.5	398	2	A98068	hypothetical prote
137	5	62.5	399	2	T10002	DNA-directed DNA p
138	5	62.5	399	2	G71314	conserved hypothet
139	5	62.5	402	2	F70850	DNA-directed DNA p
140	5	62.5	403	2	AC1743	NADH dehydrogenase
141	5	62.5	404	2	AD2170	histidyl-tRNA synt
142	5	62.5	415	2	S74041	pyruvate synthase
143	5	62.5	416	2	T44842	probable UDPglucos
144	5	62.5	418	2	H71331	probable cell divi
145	5	62.5	419	1	A45397	DNA ligase (ATP) (
146	5	62.5	419	2	S23018	DNA ligase (ATP) (
147	5	62.5	426	2	T00848	probable serine/th
148	5	62.5	426	2	H84349	peroxidase / catal
149	5	62.5	427	2	G84375	adenosylhomocystei
150	5	62.5	432	2	A70794	probable gshA prot
151	5	62.5	434	2	S23762	dihydroorotate oxi
152	5	62.5	434	2	S72430	transcription elon
153	5	62.5	434	2	D88305	protein R03D7.4 [i
154	5	62.5	434	2	B81716	hypothetical prote
155	5	62.5	439	2	F69216	conserved hypothet
156	5	62.5	442	2	S73472	probable thiophene
157	5	62.5	448	2	G83094	UDP-N-acetylmuramo
158	5	62.5	454	2	T49300	hypothetical prote
159	5	62.5	455	2	AD2620	miaB protein [impo
160	5	62.5	457	2	T25612	hypothetical prote
161	5	62.5	462	2	T26515	hypothetical prote
162	5	62.5	466	2	H71207	hypothetical prote
163	5	62.5	467	2	D97402	hypothetical 53.7K
164	5	62.5	471	2	E64325	amidophosphoribosy
165	5	62.5	481	2	H71084	hypothetical prote
166	5	62.5	483	2	AH3265	aspartate ammonia-
167	5	62.5	490	2	A87672	tldD protein [impo
168	5	62.5	494	1	F69355	Na+/H+ antiporter
169	5	62.5	496	2	B41322	N-acetylmuramoyl-L
170	5	62.5	497	2	H71516	glycine hydroxymet
171	5	62.5	497	2	C81672	serine hydroxymeth
172	5	62.5	497	2	S41014	UMP synthase - Cae
173	5	62.5	499	2	S75722	Mg-protoporphyrin
174	5	62.5	500	2	C69428	hypothetical prote
175	5	62.5	504	2	C86470	hypothetical prote
176	5	62.5	514	2	T39458	DNA binding protei
177	5	62.5	518	2	B64449	2-isopropylmalate
178	5	62.5	519	2	S78089	G-protein signalin
179	5	62.5	530	2	H86668	asparagine synthet
180	5	62.5	533	2	T31002	hypothetical prote
181	5	62.5	535	2	G97255	CTP synthase (UTP-
182	5	62.5	538	2	AG3295	phosphoglycerate d
183	5	62.5	546	2	F87343	ABC transporter, A
184	5	62.5	550	2	AD3494	oligopeptide trans

185	5	62.5	554	2	B85072	hypothetical prote
186	5	62.5	555	2	T22184	hypothetical prote
187	5	62.5	570	2	T26495	hypothetical prote
188	5	62.5	570	2	A97089	hypothetical prote
189	5	62.5	572	2	T26514	hypothetical prote
190	5	62.5	576	1	A45049	4-alpha-glucanotra
191	5	62.5	579	2	G75142	abc transporter, A
192	5	62.5	580	2	C71182	probable ABC trans
193	5	62.5	582	2	D96003	ABC transporter AT
194	5	62.5	591	2	S40816	65.4K GTP-binding
195	5	62.5	597	2	B82881	hypothetical prote
196	5	62.5	607	2	A91228	probable GTP-bindi
197	5	62.5	607	2	H86074	probable GTP-bindi
198	5	62.5	607	2	AC0004	probable GTPase bi
199	5	62.5	607	2	AH0949	GTP-binding protei
200	5	62.5	611	2	T27820	hypothetical prote
201	5	62.5	615	2	AF2972	rhizobiacin secret
202	5	62.5	615	2	E98310	rhizobiacin secret
203	5	62.5	619	2	F96703	unknown protein, 3
204	5	62.5	626	2	AF0358	conserved hypothet
205	5	62.5	626	2	T10237	RNA helicase RH16
206	5	62.5	635	2	JC5896	killer cell inhibi
207	5	62.5	637	2	S75772	hypothetical prote
208	5	62.5	644	2	A43370	capsid protein - N
209	5	62.5	646	2	S54123	neurofilament prot
210	5	62.5	672	2	H86169	hypothetical prote
211	5	62.5	680	2	JC5895	killer cell inhibi
212	5	62.5	714	2	G97230	recQ protein, supe
213	5	62.5	720	1	A48723	replication licens
214	5	62.5	725	1	Z2BPA4	rapid lysis protei
215	5	62.5	739	2	I40715	malate synthase (E
216	5	62.5	742	2	H83529	siderophore recept
217	5	62.5	750	2	AG3008	polyketide synthet
218	5	62.5	753	2	AI1339	maltosephosphoryla
219	5	62.5	759	2	T39468	anthranilate synth
220	5	62.5	759	2	T46566	anthranilate synth
221	5	62.5	770	2	F98275	saframycin mxl syn
222	5	62.5	779	2	T39584	hypothetical prote
223	5	62.5	783	2	T38690	probable regulator
224	5	62.5	788	2	C97917	exonuclease V [imp
225	5	62.5	790	2	A82200	cation transport A
226	5	62.5	790	2	G82756	conserved hypothet
227	5	62.5	793	2	S59067	penton long fiber
228	5	62.5	794	1	S37606	SEC18 protein - ye
229	5	62.5	796	2	T36308	probable integral
230	5	62.5	802	2	JH0595	potassium channel
231	5	62.5	808	2	G86208	protein F22G5.28 [
232	5	62.5	819	2	AH0056	aspartate kinase (
233	5	62.5	823	2	A96501	hypothetical prote
234	5	62.5	827	2	T40394	conserved hypothet
235	5	62.5	829	1	DJBPT5	DNA-directed DNA p
236	5	62.5	837	2	T23946	hypothetical prote
237	5	62.5	841	2	JC5894	killer cell inhibi
238	5	62.5	843	2	T22182	hypothetical prote
239	5	62.5	845	1	S34027	replication licens
240	5	62.5	846	2	E81328	probable periplasm
241	5	62.5	849	2	E86306	Similar to tufteli

242	5	62.5	863	2	D70770	probable glycogen
243	5	62.5	868	2	S76777	aconitate hydratase
244	5	62.5	874	2	JC4930	S-layer protein pr
245	5	62.5	877	2	G70934	hypothetical prote
246	5	62.5	882	2	A42855	N-heparan sulfate
247	5	62.5	882	2	A57169	[heparan sulfate]-
248	5	62.5	883	2	A49733	[heparan sulfate]-
249	5	62.5	886	1	GNLJSP	pol polyprotein -
250	5	62.5	889	2	T29590	hypothetical prote
251	5	62.5	933	2	T25600	hypothetical prote
252	5	62.5	955	2	T21612	hypothetical prote
253	5	62.5	976	2	B87291	2-oxoglutarate deh
254	5	62.5	988	2	S77211	isoleucine-tRNA li
255	5	62.5	1008	2	G82732	hypothetical prote
256	5	62.5	1017	2	A37227	Na+/K+-exchanging
257	5	62.5	1034	2	A36108	integrin alpha-V c
258	5	62.5	1042	2	T13647	hypothetical prote
259	5	62.5	1042	2	A97209	spoIID-like domain
260	5	62.5	1047	2	T51800	sucrose-phosphate
261	5	62.5	1049	2	A27079	fibronectin recept
262	5	62.5	1053	2	S44250	integrin alpha-5 c
263	5	62.5	1072	2	A38457	integrin alpha-6 c
264	5	62.5	1100	2	T47940	hypothetical prote
265	5	62.5	1127	2	T32404	hypothetical prote
266	5	62.5	1131	2	T16217	hypothetical prote
267	5	62.5	1132	2	T45037	hypothetical prote
268	5	62.5	1178	2	C71350	probable DNA-direc
269	5	62.5	1179	2	G95144	conserved hypothet
270	5	62.5	1251	2	B86194	hypothetical prote
271	5	62.5	1276	2	B86546	polymorphic outer
272	5	62.5	1276	2	C81591	polymorphic membra
273	5	62.5	1405	2	T40607	probable dna-direc
274	5	62.5	1407	2	B72078	polymorphic outer
275	5	62.5	1566	2	T20058	hypothetical prote
276	5	62.5	1735	1	S22812	DNA-directed RNA p
277	5	62.5	1815	2	B95942	conserved hypothet
278	5	62.5	1852	2	JC5546	chitin synthase (E
279	5	62.5	2028	2	T08025	DNA-directed RNA p
280	5	62.5	2364	2	I40884	cytotoxin L - Clos
281	5	62.5	2397	1	A55535	versican precursor
282	5	62.5	2588	2	T14342	NSD1 protein - mou
283	5	62.5	2756	2	T30183	hypothetical prote
284	5	62.5	3063	2	S55505	fatty-acid synthas
285	5	62.5	3450	2	T26963	hypothetical prote
286	5	62.5	3461	2	T26964	hypothetical prote
287	5	62.5	3562	2	A47171	chondroitin sulfat
288	5	62.5	3600	2	D86161	F1003.12 protein -
289	5	62.5	3660	1	S02041	dystrophin, muscle
290	5	62.5	3678	2	S28916	dystrophin - mouse
291	5	62.5	3685	1	A27605	dystrophin, muscle
292	5	62.5	4085	2	S28600	hypothetical prote
293	5	62.5	4342	2	H83343	probable non-ribos
294	5	62.5	4725	1	A44357	dynein heavy chain
295	4	50.0	15	2	PQ0017	terminal protein -
296	4	50.0	17	2	I55226	myosin heavy chain
297	4	50.0	30	2	S27306	surface layer prot
298	4	50.0	32	2	G31485	Ig heavy chain V r

299	4	50.0	33	2	S23094	beta-amyloid prote
300	4	50.0	33	2	H95094	hypothetical prote
301	4	50.0	33	2	E82852	hypothetical prote
302	4	50.0	39	2	S67938	hypothetical prote
303	4	50.0	42	2	PN0512	beta-amyloid prote
304	4	50.0	49	2	T07309	hypothetical prote
305	4	50.0	50	2	S41323	8K protein - potat
306	4	50.0	50	2	B85894	hypothetical prote
307	4	50.0	53	2	S43965	hypothetical prote
308	4	50.0	53	2	E64365	hypothetical prote
309	4	50.0	54	2	C72809	gp87 protein - Myc
310	4	50.0	55	2	S66320	protein kinase AK7
311	4	50.0	56	2	H81353	hypothetical prote
312	4	50.0	57	2	I68807	MHC class II histo
313	4	50.0	57	2	E60045	Alzheimer's diseas
314	4	50.0	57	2	F60045	Alzheimer's diseas
315	4	50.0	57	2	G60045	Alzheimer's diseas
316	4	50.0	57	2	D60045	Alzheimer's diseas
317	4	50.0	57	2	A60045	Alzheimer's diseas
318	4	50.0	57	2	B60045	Alzheimer's diseas
319	4	50.0	57	2	S66319	protein kinase AK6
320	4	50.0	59	2	A69520	hypothetical prote
321	4	50.0	59	2	T38172	hypothetical prote
322	4	50.0	61	2	H82090	hypothetical prote
323	4	50.0	62	2	S45295	cyclin Cyc3 - Arab
324	4	50.0	62	2	T02777	y4dN protein - Rhi
325	4	50.0	62	2	S27308	surface layer prot
326	4	50.0	63	2	S04973	antifreeze protein
327	4	50.0	63	2	D42194	petH protein - Syn
328	4	50.0	64	1	QABP22	restriction inhibi
329	4	50.0	65	2	AB3381	heavy metal bindin
330	4	50.0	66	2	S10561	chlorophyll a/b-bi
331	4	50.0	66	2	T35138	hypothetical prote
332	4	50.0	66	2	C95310	hypothetical prote
333	4	50.0	66	2	AH3266	hypothetical prote
334	4	50.0	67	2	F90956	probable DNA-bindi
335	4	50.0	67	2	T40218	probable ATP synth
336	4	50.0	67	2	B85805	probable regulator
337	4	50.0	68	2	A88030	protein F46F5.8 [i
338	4	50.0	68	2	C82492	hypothetical prote
339	4	50.0	70	1	WMWGP4	8K protein - potat
340	4	50.0	70	2	S58932	DNA-directed RNA p
341	4	50.0	71	2	B64479	hypothetical prote
342	4	50.0	71	2	AB2819	hypothetical prote
343	4	50.0	72	2	S34404	ribosomal protein
344	4	50.0	72	2	T30373	hypothetical prote
345	4	50.0	72	2	E69386	hypothetical prote
346	4	50.0	72	2	C89933	hypothetical prote
347	4	50.0	73	2	H90802	hypothetical prote
348	4	50.0	73	2	AI3065	hypothetical prote
349	4	50.0	73	2	G98220	hypothetical prote
350	4	50.0	74	2	AH1317	ferredoxin homolog
351	4	50.0	74	2	AH1689	ferredoxin homolog
352	4	50.0	74	2	B90864	phage shock protei
353	4	50.0	74	2	G85754	phage shock protei
354	4	50.0	74	2	S17122	phage shock protei
355	4	50.0	74	2	E81284	hypothetical prote

356	4	50.0	74	2	AG0658	phage shock protei
357	4	50.0	75	1	BVECRY	traY protein - Esc
358	4	50.0	75	2	A99609	hypothetical prote
359	4	50.0	75	2	H81320	small hydrophobic
360	4	50.0	76	2	T25127	hypothetical prote
361	4	50.0	77	2	F69219	conserved hypothet
362	4	50.0	77	2	C69359	snRNP homolog - Ar
363	4	50.0	79	2	S38756	cytochrome c551 -
364	4	50.0	79	2	S31013	gene 68 protein -
365	4	50.0	79	2	T17694	hypothetical prote
366	4	50.0	80	2	JE0277	fracture callus pr
367	4	50.0	80	2	T31267	4-oxalocrotonoate
368	4	50.0	80	2	H89990	hypothetical prote
369	4	50.0	81	2	B91000	hypothetical prote
370	4	50.0	82	2	I36924	gene MHC DQ-beta 1
371	4	50.0	82	2	I61815	gene MHC DQ-beta 1
372	4	50.0	82	2	I61818	gene MHC DQ-beta 1
373	4	50.0	82	2	I61834	gene MHC DQ-beta 1
374	4	50.0	82	2	PQ0438	Alzheimer's diseas
375	4	50.0	82	2	JC4205	hypothetical 9.1k
376	4	50.0	82	2	T09234	hypothetical prote
377	4	50.0	82	2	AB0272	hypothetical prote
378	4	50.0	82	2	C97597	hypothetical prote
379	4	50.0	83	2	T36483	probable membrane
380	4	50.0	83	2	AC0270	conserved hypothet
381	4	50.0	84	2	S43801	hypothetical prote
382	4	50.0	84	2	H83549	conserved hypothet
383	4	50.0	84	2	E70841	hypothetical prote
384	4	50.0	85	1	GDEC	glutaredoxin 1 - E
385	4	50.0	85	2	A99745	hypothetical prote
386	4	50.0	85	2	E85595	hypothetical prote
387	4	50.0	85	2	B75389	hypothetical prote
388	4	50.0	85	2	T47563	kinetochore-like p
389	4	50.0	86	2	A97846	hypothetical prote
390	4	50.0	87	2	B97814	hypothetical prote
391	4	50.0	88	2	JS0644	eclosion hormone p
392	4	50.0	88	2	A38085	S-layer glycoprote
393	4	50.0	89	2	S54814	probable acyl carr
394	4	50.0	89	2	A90820	hypothetical prote
395	4	50.0	89	2	H87367	hypothetical prote
396	4	50.0	89	2	A70224	conserved hypothet
397	4	50.0	89	2	E97731	hypothetical prote
398	4	50.0	90	1	S01373	ribonuclease inhib
399	4	50.0	90	2	S45083	hypothetical prote
400	4	50.0	90	2	T46007	hypothetical prote
401	4	50.0	91	1	C69973	ribonuclease inhib
402	4	50.0	91	1	BVECAC	racC protein - Esc
403	4	50.0	91	2	A97004	barstar-like prote
404	4	50.0	91	2	A55406	calgranulin c - pi
405	4	50.0	91	2	B85748	hypothetical prote
406	4	50.0	91	2	G90870	racC protein [impo
407	4	50.0	91	2	T29686	hypothetical prote
408	4	50.0	91	2	AI1583	hypothetical prote
409	4	50.0	93	2	G81410	hydrogenase isoenz
410	4	50.0	93	2	AB0449	probable ribonucle
411	4	50.0	94	2	I79418	MHC HLA-DRQ-beta c
412	4	50.0	94	2	S23685	erythrocyte membra

413	4	50.0	94	2	E97759	hypothetical prote
414	4	50.0	95	2	A81176	ribonuclease inhib
415	4	50.0	95	2	D69121	hypothetical prote
416	4	50.0	96	2	A57483	3-mercaptopyruvate
417	4	50.0	96	2	PC4086	ribosomal protein
418	4	50.0	96	2	H36850	A25L protein - var
419	4	50.0	96	2	T28567	hypothetical prote
420	4	50.0	97	2	H84901	hypothetical prote
421	4	50.0	97	2	S72857	hypothetical prote
422	4	50.0	97	2	AC1397	conserved hypothet
423	4	50.0	97	2	AH2901	conserved hypothet
424	4	50.0	97	2	B97677	hypothetical prote
425	4	50.0	99	2	I40317	DNA repair protein
426	4	50.0	99	2	B95115	hypothetical prote
427	4	50.0	99	2	T06983	root abundant prot
428	4	50.0	99	2	B97409	hypothetical prote
429	4	50.0	100	2	AI2298	cobalt transport p
430	4	50.0	100	2	G98295	hypothetical prote
431	4	50.0	101	2	S51162	protein kinase PRK
432	4	50.0	101	2	E87643	conserved hypothet
433	4	50.0	101	2	T25255	hypothetical prote
434	4	50.0	102	2	C84026	ribosomal protein
435	4	50.0	102	2	S37565	chaperonin groES -
436	4	50.0	102	2	A41325	heat shock protein
437	4	50.0	102	2	C84003	exogenous DNA-bind
438	4	50.0	102	2	A87573	hypothetical prote
439	4	50.0	103	2	S36539	E7 protein - human
440	4	50.0	103	2	S77343	carbon dioxide con
441	4	50.0	103	2	T03013	hypothetical prote
442	4	50.0	103	2	A85821	unknown protein en
443	4	50.0	103	2	E90973	hypothetical prote
444	4	50.0	103	2	E72664	hypothetical prote
445	4	50.0	104	2	A69407	signal recognition
446	4	50.0	104	2	E86263	F13K23.22 protein
447	4	50.0	105	2	T42021	Ser/Thr protein ph
448	4	50.0	105	2	B70716	hypothetical prote
449	4	50.0	105	2	AD2301	hypothetical prote
450	4	50.0	106	2	AI0113	probable Rieske pr
451	4	50.0	106	2	JG0021	flagellar hook-bas
452	4	50.0	107	2	AC3392	hypothetical cytos
453	4	50.0	108	1	S02802	thioredoxin C-2 -
454	4	50.0	108	2	S53658	hydrogenase-relate
455	4	50.0	109	2	S77444	hypothetical prote
456	4	50.0	109	2	S50356	sugar transport pr
457	4	50.0	109	2	B64145	hypothetical prote
458	4	50.0	109	2	G69276	conserved hypothet
459	4	50.0	109	2	B70637	hypothetical prote
460	4	50.0	109	2	F97132	hypothetical prote
461	4	50.0	111	1	A32233	thioredoxin 2 [val
462	4	50.0	111	2	E72524	probable ribosomal
463	4	50.0	112	2	A69451	conserved hypothet
464	4	50.0	112	2	A75544	conserved hypothet
465	4	50.0	112	2	B95061	BlpS protein [impo
466	4	50.0	112	2	F97929	regulatory protein
467	4	50.0	112	2	C55993	hypothetical prote
468	4	50.0	112	2	T39864	hypothetical prote
469	4	50.0	113	2	A72380	nitrogen regulator

470	4	50.0	113	2	T41404	hypothetical prote
471	4	50.0	113	2	D70586	hypothetical prote
472	4	50.0	113	2	E64309	hypothetical prote
473	4	50.0	113	2	C83893	hypothetical prote
474	4	50.0	114	2	PH1027	Ig heavy chain V r
475	4	50.0	114	2	AF0252	conserved hypothet
476	4	50.0	114	2	AG0725	conserved hypothet
477	4	50.0	114	2	D64345	hypothetical prote
478	4	50.0	114	2	H89785	hypothetical prote
479	4	50.0	115	2	AF2098	thioredoxin 2 [imp
480	4	50.0	115	2	T48186	light-inducible pr
481	4	50.0	115	2	D32227	hypothetical prote
482	4	50.0	115	2	B70536	hypothetical prote
483	4	50.0	115	2	E84340	hypothetical prote
484	4	50.0	115	2	E97483	hypothetical prote
485	4	50.0	116	1	NGNJXI	nerve growth facto
486	4	50.0	116	1	R5HSH9	ribosomal protein
487	4	50.0	116	2	A58566	nerve growth facto
488	4	50.0	116	2	T44504	merP protein [impo
489	4	50.0	116	2	T45512	probable transport
490	4	50.0	116	2	C64562	hypothetical prote
491	4	50.0	116	2	G64126	N-acetylmuramoyl-L
492	4	50.0	116	2	E83374	hypothetical prote
493	4	50.0	116	2	T01231	hypothetical prote
494	4	50.0	116	2	JQ1283	hypothetical 13.9K
495	4	50.0	116	2	AG3446	arsenate reductase
496	4	50.0	116	2	AG3102	conserved hypothet
497	4	50.0	117	1	T43941	ribosomal protein
498	4	50.0	117	2	T12708	thioredoxin-disulf
499	4	50.0	117	2	E84269	50S ribosomal prot
500	4	50.0	117	2	F64708	conserved hypothet
501	4	50.0	118	2	S27187	multidrug resistan
502	4	50.0	118	2	F83138	hypothetical prote
503	4	50.0	118	2	T26804	hypothetical prote
504	4	50.0	119	2	A36724	hypothetical prote
505	4	50.0	119	2	E70799	hypothetical prote
506	4	50.0	119	2	T17032	fimbriata-associat
507	4	50.0	119	2	H82193	hypothetical prote
508	4	50.0	119	2	B95226	hypothetical prote
509	4	50.0	119	2	E98090	hypothetical prote
510	4	50.0	120	2	F72557	probable ribosomal
511	4	50.0	120	2	D75360	hypothetical prote
512	4	50.0	120	2	B95269	probable sensory t
513	4	50.0	121	2	D27888	Ig heavy chain V r
514	4	50.0	121	2	E95027	ribosomal protein
515	4	50.0	121	2	E97898	30S ribosomal prot
516	4	50.0	121	2	AG1776	ribosomal protein
517	4	50.0	121	2	AH1400	ribosomal protein
518	4	50.0	121	2	S78265	ribosomal protein
519	4	50.0	121	2	D95132	conserved hypothet
520	4	50.0	121	2	G75604	hypothetical prote
521	4	50.0	122	2	H30535	Ig heavy chain V r
522	4	50.0	123	2	S55326	pseudoazurin - Thi
523	4	50.0	123	2	C81004	hypothetical prote
524	4	50.0	123	2	E89930	conserved hypothet
525	4	50.0	124	2	C24733	myosin alpha heavy
526	4	50.0	124	2	D81105	conserved hypothet

527	4	50.0	124	2	JC1180	tylosin-resistance
528	4	50.0	124	2	B87345	hypothetical prote
529	4	50.0	124	2	H81005	adhesin complex pr
530	4	50.0	124	2	A81910	hypothetical prote
531	4	50.0	124	2	A30043	trophoblast-specif
532	4	50.0	124	2	AC2604	PilQ [imported] -
533	4	50.0	125	2	I40847	succinate dehydrog
534	4	50.0	125	2	AD1180	conserved hypothet
535	4	50.0	125	2	S07739	hypothetical prote
536	4	50.0	125	2	A60426	high molecular wei
537	4	50.0	125	2	C86046	hypothetical prote
538	4	50.0	125	2	G91199	hypothetical prote
539	4	50.0	125	2	C98286	hypothetical prote
540	4	50.0	126	2	S53340	CD59 protein - rat
541	4	50.0	126	2	C64155	hypothetical prote
542	4	50.0	126	2	AD2313	hypothetical prote
543	4	50.0	127	2	B64034	hypothetical prote
544	4	50.0	127	2	F82617	ferredoxin XF1964
545	4	50.0	127	2	AG1425	hypothetical secre
546	4	50.0	128	2	C83448	succinate dehydrog
547	4	50.0	128	2	B83268	hypothetical prote
548	4	50.0	128	2	B72600	hypothetical prote
549	4	50.0	129	1	DEECS4	succinate dehydrog
550	4	50.0	129	2	B90722	succinate dehydrog
551	4	50.0	129	2	A85573	succinate dehydrog
552	4	50.0	129	2	AE0136	succinate dehydrog
553	4	50.0	129	2	AH0590	succinate dehydrog
554	4	50.0	129	2	A60869	nif-specific regul
555	4	50.0	129	2	AE1933	hypothetical prote
556	4	50.0	129	2	H86673	single-strand bind
557	4	50.0	129	2	D82627	hypothetical prote
558	4	50.0	129	2	AC0782	probable DNA-bindi
559	4	50.0	130	2	A82119	succinate dehydrog
560	4	50.0	130	2	S06817	Ig heavy chain V r
561	4	50.0	130	2	B85792	hypothetical prote
562	4	50.0	130	2	F90943	hypothetical prote
563	4	50.0	130	2	A64942	hypothetical prote
564	4	50.0	130	2	F69434	conserved hypothet
565	4	50.0	130	2	F83129	5-carboxymethyl-2-
566	4	50.0	130	2	T34729	probable gas vesic
567	4	50.0	131	1	SIPSDP	steroid Delta-isom
568	4	50.0	131	2	S30956	gene 11 protein -
569	4	50.0	131	2	T49454	hypothetical prote
570	4	50.0	131	2	T22997	hypothetical prote
571	4	50.0	132	2	S57744	adipocyte-type fat
572	4	50.0	132	2	T44759	glycine cleavage s
573	4	50.0	132	2	H97011	uncharacterized co
574	4	50.0	132	2	B85092	hypothetical prote
575	4	50.0	133	2	D70105	hypothetical prote
576	4	50.0	133	2	B70848	hypothetical prote
577	4	50.0	133	2	E90496	hypothetical prote
578	4	50.0	133	2	E69338	hypothetical prote
579	4	50.0	133	2	AI2987	hypothetical prote
580	4	50.0	134	2	B84246	cytidine aminohydr
581	4	50.0	134	2	S03474	T-cell receptor al
582	4	50.0	134	2	AF3280	SSU ribosomal prot
583	4	50.0	134	2	C70721	probable gcvH prot

584	4	50.0	134	2	S76180	hypothetical prote
585	4	50.0	134	2	G72166	A26L protein - var
586	4	50.0	134	2	F97984	hypothetical prote
587	4	50.0	135	2	G83495	hypothetical prote
588	4	50.0	136	2	T36606	heat shock protein
589	4	50.0	136	2	PC2225	peptide L1AE 3 - p
590	4	50.0	136	2	A90710	regulator of nucle
591	4	50.0	136	2	E85560	regulator of nucle
592	4	50.0	136	2	AG0449	regulator of nucle
593	4	50.0	136	2	I57917	nucleoside diphosp
594	4	50.0	136	2	AC0578	regulator of nucle
595	4	50.0	136	2	B97386	hypothetical prote
596	4	50.0	137	1	F69319	conserved hypothet
597	4	50.0	137	2	H84218	hypothetical prote
598	4	50.0	137	2	H82537	TonB protein XF260
599	4	50.0	138	2	T34802	hypothetical prote
600	4	50.0	138	2	B45277	probable transposi
601	4	50.0	138	2	C72713	hypothetical prote
602	4	50.0	138	2	A82674	virulence regulato
603	4	50.0	138	2	T16053	hypothetical prote
604	4	50.0	139	2	B64324	ribosomal protein
605	4	50.0	139	2	A69052	riboflavin synthas
606	4	50.0	139	2	D81364	probable periplasm
607	4	50.0	139	2	T27115	hypothetical prote
608	4	50.0	139	2	E85845	unknown protein en
609	4	50.0	139	2	G87625	FliJ protein [impo
610	4	50.0	140	2	S72252	hemoglobin, extrac
611	4	50.0	140	2	B81431	hypothetical prote
612	4	50.0	140	2	E70632	hypothetical prote
613	4	50.0	141	2	E81294	50S ribosomal prot
614	4	50.0	141	2	AC1994	hypothetical prote
615	4	50.0	141	2	T46748	hypothetical prote
616	4	50.0	141	2	D97172	uncharacterized pr
617	4	50.0	142	2	T08343	arsC protein - Hal
618	4	50.0	142	2	AB0138	TolR colicin impor
619	4	50.0	142	2	A87501	hypothetical prote
620	4	50.0	142	2	E89026	protein F13A2.1 [i
621	4	50.0	142	2	AB0624	probable bacteriop
622	4	50.0	142	2	B97631	hypothetical prote
623	4	50.0	143	2	E90265	conserved hypothet
624	4	50.0	143	2	JN0093	hypothetical 17K p
625	4	50.0	144	2	F87538	ExbD/TolR family p
626	4	50.0	144	2	S75520	hypothetical prote
627	4	50.0	144	2	F71708	hypothetical prote
628	4	50.0	144	2	B95048	transcription regu
629	4	50.0	144	2	B95242	hypothetical prote
630	4	50.0	144	2	G90913	hypothetical prote
631	4	50.0	144	2	B75284	MutT/nudix family
632	4	50.0	144	2	H97918	conserved hypothet
633	4	50.0	144	2	E98106	conserved hypothet
634	4	50.0	145	2	S62510	hypothetical prote
635	4	50.0	145	2	B96705	unknown protein, 8
636	4	50.0	145	2	C49683	pts 3'-region prot
637	4	50.0	146	1	A48897	aminoglycoside N6'
638	4	50.0	146	1	R5BSL5	ribosomal protein
639	4	50.0	146	1	QXBP4L	hypothetical prote
640	4	50.0	146	2	S71256	ribosomal protein

641	4	50.0	146	2	H95026	ribosomal protein
642	4	50.0	146	2	B90020	50S ribosomal prot
643	4	50.0	146	2	H97897	50S ribosomal prot
644	4	50.0	146	2	AD1777	ribosomal protein
645	4	50.0	146	2	AE1401	ribosomal protein
646	4	50.0	146	2	H75495	conserved hypothet
647	4	50.0	146	2	E64001	hypothetical prote
648	4	50.0	146	2	E75289	probable phenylace
649	4	50.0	146	2	AF2500	hypothetical prote
650	4	50.0	147	2	S60875	phosphorylation-ac
651	4	50.0	147	2	S40703	G10 protein homolo
652	4	50.0	148	1	R5RTLA	ribosomal protein
653	4	50.0	148	1	R5MS27	ribosomal protein
654	4	50.0	148	2	S25593	60s ribosomal prot
655	4	50.0	148	2	S55914	ribosomal protein
656	4	50.0	148	2	S60001	60s ribosomal prot
657	4	50.0	148	2	AB1798	phosphotransferase
658	4	50.0	148	2	AD1424	phosphotransferase
659	4	50.0	148	2	F87666	conserved hypothet
660	4	50.0	148	2	T08352	hypothetical prote
661	4	50.0	148	2	E82434	hypothetical prote
662	4	50.0	148	2	B85641	hypothetical prote
663	4	50.0	148	2	C90780	hypothetical prote
664	4	50.0	149	2	D84292	transcription regu
665	4	50.0	149	2	C64335	conserved hypothet
666	4	50.0	149	2	B81749	conserved hypothet
667	4	50.0	149	2	D83560	probable type II s
668	4	50.0	149	2	T43637	caspase protein 1C
669	4	50.0	150	2	S29890	Ribosomal protein
670	4	50.0	150	2	S18435	troponin C isoform
671	4	50.0	150	2	AD3155	transcription regu
672	4	50.0	150	2	E98132	probable transcrip
673	4	50.0	150	2	G84585	probable kinetecho
674	4	50.0	150	2	C83329	hypothetical prote
675	4	50.0	150	2	B87677	hypothetical prote
676	4	50.0	150	2	AI1968	hypothetical prote
677	4	50.0	150	2	F83018	hypothetical prote
678	4	50.0	151	2	S50005	ribosomal protein
679	4	50.0	151	2	S60870	phosphorylation-ac
680	4	50.0	151	2	A69539	maoC protein (maoC
681	4	50.0	151	2	E64167	yabB protein homol
682	4	50.0	151	2	T42950	hypothetical prote
683	4	50.0	151	2	T35840	probable membrane
684	4	50.0	151	2	T28645	transcription fact
685	4	50.0	151	2	JN0521	toxin co-regulated
686	4	50.0	151	2	AD2274	hypothetical prote
687	4	50.0	151	2	E70615	hypothetical prote
688	4	50.0	151	2	AH3221	conserved hypothet
689	4	50.0	152	2	I47188	Ig heavy chain var
690	4	50.0	152	2	S14388	yabB protein - Esc
691	4	50.0	152	2	E90639	hypothetical prote
692	4	50.0	152	2	E85490	hypothetical prote
693	4	50.0	152	2	AG0067	conserved hypothet
694	4	50.0	152	2	AD0517	conserved hypothet
695	4	50.0	152	2	H71129	hypothetical prote
696	4	50.0	152	2	T08718	hypothetical prote
697	4	50.0	152	2	C98184	hypothetical prote

698	4	50.0	153	1	S73839	MG230 homolog F10_
699	4	50.0	153	2	T44263	tRNA-pseudouridine
700	4	50.0	153	2	A95928	probable amine oxi
701	4	50.0	153	2	G72476	hypothetical prote
702	4	50.0	153	2	AG2125	hypothetical prote
703	4	50.0	154	1	H69532	conserved hypothet
704	4	50.0	154	2	AI3307	leucine-responsive
705	4	50.0	154	2	B75324	conserved hypothet
706	4	50.0	154	2	T47825	Skp1-like protein
707	4	50.0	154	2	T38823	hypothetical prote
708	4	50.0	155	2	A29699	beta-lactoglobulin
709	4	50.0	155	2	H81363	probable RNA methy
710	4	50.0	155	2	T33008	hypothetical prote
711	4	50.0	155	2	T21364	hypothetical prote
712	4	50.0	155	2	PQ0515	hypothetical prote
713	4	50.0	155	2	AB2851	conserved hypothet
714	4	50.0	155	2	H97627	hypothetical prote
715	4	50.0	156	2	AB3349	LSU ribosomal prot
716	4	50.0	156	2	H95844	probable transcrip
717	4	50.0	156	2	AG1536	hypothetical prote
718	4	50.0	156	2	C96023	probable C-P (carb
719	4	50.0	156	2	B83361	probable transcrip
720	4	50.0	156	2	B64036	hypothetical prote
721	4	50.0	156	2	D70541	hypothetical prote
722	4	50.0	157	2	AI1341	PTS system, fructo
723	4	50.0	157	2	S22489	IgE-dependent hist
724	4	50.0	157	2	AE1104	B. subtilis YacN p
725	4	50.0	157	2	AE1466	B. subtilis YacN p
726	4	50.0	157	2	H69203	conserved hypothet
727	4	50.0	157	2	E87037	probable membrane
728	4	50.0	157	2	G64135	hypothetical prote
729	4	50.0	157	2	B86917	hypothetical prote
730	4	50.0	157	2	AE1283	hypothetical prote
731	4	50.0	158	2	D83384	probable transcrip
732	4	50.0	158	2	S53572	probable membrane
733	4	50.0	158	2	E72659	hypothetical prote
734	4	50.0	158	2	D87384	hypothetical prote
735	4	50.0	158	2	D97642	hypothetical prote
736	4	50.0	158	2	AF2865	conserved hypothet
737	4	50.0	158	2	E90198	hypothetical prote
738	4	50.0	159	2	T30445	hypothetical prote
739	4	50.0	159	2	D69150	conserved hypothet
740	4	50.0	159	2	F87218	conserved hypothet
741	4	50.0	159	2	AG1090	hypothetical prote
742	4	50.0	159	2	JE0031	nitrogenase (EC 1.
743	4	50.0	160	1	A38177	flavodoxin - Clost
744	4	50.0	160	2	AI1308	dihydrofolate redu
745	4	50.0	160	2	AI1680	dihydrofolate redu
746	4	50.0	160	2	A64136	molybdenum cofacto
747	4	50.0	160	2	F64003	hypothetical prote
748	4	50.0	160	2	T18780	hypothetical prote
749	4	50.0	160	2	AC2958	conserved hypothet
750	4	50.0	160	2	H88114	protein F53C3.6 [i
751	4	50.0	160	2	H86538	SS DNA binding pro
752	4	50.0	160	2	G64692	restriction modifi
753	4	50.0	160	2	H72083	single-strand bind
754	4	50.0	161	1	G64814	molybdenum cofacto

755	4	50.0	161	2	D87406	ribosomal protein
756	4	50.0	161	2	E90736	molybdenum cofacto
757	4	50.0	161	2	F85586	molybdopterin bios
758	4	50.0	161	2	T35369	hypothetical prote
759	4	50.0	161	2	AC3263	emg2 protein [impo
760	4	50.0	161	2	D70040	hypothetical prote
761	4	50.0	161	2	E70530	hypothetical prote
762	4	50.0	161	2	T21405	hypothetical prote
763	4	50.0	161	2	T48285	hypothetical prote
764	4	50.0	161	2	E89007	protein F59B1.2 [i
765	4	50.0	162	2	A34429	dihydrofolate redu
766	4	50.0	162	2	T18188	hypothetical prote
767	4	50.0	162	2	F96496	probable myosin he
768	4	50.0	163	2	B48766	ubiquitin-like pro
769	4	50.0	163	2	AE2854	conserved hypothet
770	4	50.0	164	2	B35127	phycoerythrin alph
771	4	50.0	164	2	C83948	hypothetical prote
772	4	50.0	164	2	C98325	probable transcrip
773	4	50.0	164	2	T11215	hypothetical prote
774	4	50.0	165	2	H84293	hypothetical prote
775	4	50.0	165	2	B83703	hypothetical prote
776	4	50.0	166	1	S07369	interleukin-3 prec
777	4	50.0	166	2	T28809	hypothetical prote
778	4	50.0	166	2	D71861	thioredoxin peroxi
779	4	50.0	166	2	F64568	thioredoxin peroxi
780	4	50.0	166	2	AC1940	purine-binding che
781	4	50.0	167	1	RDSODF	dihydrofolate redu
782	4	50.0	167	2	T09686	TCTP protein homol
783	4	50.0	167	2	B85437	caltractin-like pr
784	4	50.0	167	2	AF1906	molybdopterin prec
785	4	50.0	167	2	T22198	hypothetical prote
786	4	50.0	167	2	C84773	hypothetical prote
787	4	50.0	168	1	A38958	IgE-dependent hist
788	4	50.0	168	2	F95365	NADH2 dehydrogenas
789	4	50.0	168	2	JC6566	interleukin-3 beta
790	4	50.0	168	2	G83288	transcription elon
791	4	50.0	168	2	T47054	hypothetical prote
792	4	50.0	168	2	T14723	antirestriction pr
793	4	50.0	168	2	T34076	hypothetical prote
794	4	50.0	168	2	T12834	hypothetical prote
795	4	50.0	168	2	C90209	hypothetical prote
796	4	50.0	168	2	G86578	CT670 hypothetical
797	4	50.0	168	2	E70080	conserved hypothet
798	4	50.0	168	2	T36405	probable marR-fami
799	4	50.0	168	2	D64459	3-isopropylmalate
800	4	50.0	168	2	B72046	conserved hypothet
801	4	50.0	169	2	S77054	hypothetical prote
802	4	50.0	169	2	H82398	hypothetical prote
803	4	50.0	169	2	H83972	hypothetical prote
804	4	50.0	170	1	JN0608	phospholipid-hydro
805	4	50.0	170	1	HMECBM	M-agglutinin precu
806	4	50.0	170	2	B71864	hypothetical prote
807	4	50.0	170	2	T02707	probable kinetecho
808	4	50.0	170	2	C83481	hypothetical prote
809	4	50.0	170	2	B96725	hypothetical prote
810	4	50.0	170	2	AC0256	lysozyme (EC 3.2.1
811	4	50.0	170	2	S69465	hypothetical prote

812	4	50.0	171	2	G69077	ferritin like prot
813	4	50.0	171	2	B47125	regulatory protein
814	4	50.0	171	2	E84773	hypothetical prote
815	4	50.0	171	2	A99265	glutaredoxin relat
816	4	50.0	171	2	D86444	probable heat shoc
817	4	50.0	171	2	G84421	probable auxin-ind
818	4	50.0	172	2	H69103	VPS29-like phospho
819	4	50.0	172	2	I48171	alpha-crystallin B
820	4	50.0	172	2	S32489	lectin - Iberian r
821	4	50.0	172	2	AC0833	probable exported
822	4	50.0	172	2	T10346	hypothetical prote
823	4	50.0	173	2	I46197	cell surface prote
824	4	50.0	173	2	E84987	formylmethionine d
825	4	50.0	173	2	A46177	enhancer of split
826	4	50.0	173	2	A75512	hypothetical prote
827	4	50.0	173	2	C95850	hypothetical prote
828	4	50.0	173	2	AH3486	soluble lytic mure
829	4	50.0	174	2	A49181	alpha B-crystallin
830	4	50.0	174	2	S58758	alpha-crystallin c
831	4	50.0	174	2	S71554	pathogenesis-relat
832	4	50.0	174	2	S05574	streptothricin ace
833	4	50.0	174	2	A70337	hypothetical prote
834	4	50.0	174	2	H83481	hypothetical prote
835	4	50.0	174	2	AE2582	heat shock protein
836	4	50.0	174	2	AI0618	conserved hypothet
837	4	50.0	175	1	CYBOAB	alpha-crystallin c
838	4	50.0	175	1	CYHUAB	alpha-crystallin c
839	4	50.0	175	2	A53871	alpha-crystallin c
840	4	50.0	175	2	A39608	alpha-crystallin c
841	4	50.0	175	2	I53319	alpha B-crystallin
842	4	50.0	175	2	A23681	alpha-crystallin c
843	4	50.0	175	2	JC5971	alpha-b crystallin
844	4	50.0	175	2	D75467	bacterioferritin c
845	4	50.0	175	2	E97701	hypothetical prote
846	4	50.0	175	2	F84361	orotate phosphorib
847	4	50.0	175	2	H91177	hypothetical prote
848	4	50.0	175	2	A86024	hypothetical prote
849	4	50.0	175	2	S47732	hypothetical 20.6K
850	4	50.0	176	2	JK0226	arachin 21K chain
851	4	50.0	176	2	G81500	UDP-N-acetylglucos
852	4	50.0	177	2	T31086	probable dTDP-4-de
853	4	50.0	177	2	A33954	hypothetical prote
854	4	50.0	177	2	T37808	hypothetical prote
855	4	50.0	177	2	F95912	hypothetical prote
856	4	50.0	178	2	A95235	transcription anti
857	4	50.0	178	2	B42845	3-hydroxybutyrate
858	4	50.0	178	2	C90041	conserved hypothet
859	4	50.0	178	2	S39875	hypothetical prote
860	4	50.0	178	2	H70353	hypothetical prote
861	4	50.0	178	2	F85925	hypothetical prote
862	4	50.0	178	2	E91080	hypothetical prote
863	4	50.0	178	2	A89806	hypothetical prote
864	4	50.0	179	2	S62019	hypothetical prote
865	4	50.0	179	2	C83425	hypothetical prote
866	4	50.0	179	2	AD0259	probable phage reg
867	4	50.0	179	2	H91049	probable membrane
868	4	50.0	179	2	E85894	probable membrane

869	4	50.0	179	2	A65027	hypothetical prote
870	4	50.0	180	2	B69867	2-cys peroxiredoxi
871	4	50.0	180	2	T44944	hypothetical prote
872	4	50.0	180	2	A56836	bone marrow stroma
873	4	50.0	180	2	S70725	rec15 protein - fi
874	4	50.0	181	2	S70030	myosin heavy chain
875	4	50.0	181	2	B90246	TATA box binding p
876	4	50.0	181	2	AE3291	5-formyltetrahydro
877	4	50.0	181	2	F64743	yaeQ protein - Esc
878	4	50.0	181	2	F75561	hypothetical prote
879	4	50.0	181	2	F82235	response regulator
880	4	50.0	181	2	S73534	hypothetical prote
881	4	50.0	182	2	F64569	hypothetical prote
882	4	50.0	182	2	B90060	hypothetical prote
883	4	50.0	183	2	A83983	2-cys peroxiredoxi
884	4	50.0	183	2	T34820	deoxyuridine 5'-tr
885	4	50.0	183	2	B98099	transcription anti
886	4	50.0	183	2	S75697	hypothetical prote
887	4	50.0	183	2	D75620	hypothetical prote
888	4	50.0	183	2	D86748	hypothetical prote
889	4	50.0	183	2	T30744	hypothetical prote
890	4	50.0	183	2	T30677	hypothetical prote
891	4	50.0	184	2	T43321	ribosomal protein
892	4	50.0	184	2	F64312	phenylacrylic acid
893	4	50.0	184	2	S74574	bacterioferritin c
894	4	50.0	184	2	T17446	hypothetical 21.1K
895	4	50.0	184	2	AD0232	hypothetical prote
896	4	50.0	184	2	A64558	hypothetical prote
897	4	50.0	184	2	C71949	hypothetical prote
898	4	50.0	184	2	F72328	hypothetical prote
899	4	50.0	184	2	C72495	hypothetical prote
900	4	50.0	184	2	H75334	hypothetical prote
901	4	50.0	185	1	B69374	conserved hypothet
902	4	50.0	185	2	B69028	probable phosphono
903	4	50.0	185	2	AH3399	hypothetical cytos
904	4	50.0	185	2	B83520	hypothetical prote
905	4	50.0	186	2	E87433	conserved hypothet
906	4	50.0	186	2	T47428	hypothetical prote
907	4	50.0	186	2	D83515	hypothetical prote
908	4	50.0	186	2	C82029	probable adhesin c
909	4	50.0	186	2	T47804	hypothetical prote
910	4	50.0	186	2	T31347	hypothetical prote
911	4	50.0	187	2	H69706	RNA polymerase ECF
912	4	50.0	187	2	H75489	hypothetical prote
913	4	50.0	188	2	G82999	conserved hypothet
914	4	50.0	188	2	AE0003	conserved hypothet
915	4	50.0	189	2	T43516	ribosomal protein
916	4	50.0	189	2	C81363	4-methyl-5(beta-hy
917	4	50.0	189	2	D75339	hypothetical prote
918	4	50.0	189	2	JC7107	development relate
919	4	50.0	189	2	T00401	hypothetical prote
920	4	50.0	189	2	AD2916	transcription regu
921	4	50.0	189	2	G97690	hypothetical prote
922	4	50.0	190	2	S68230	antimicrobial pept
923	4	50.0	190	2	D84042	translation initia
924	4	50.0	190	2	JC4514	TATA-binding prote
925	4	50.0	190	2	B81386	probable periplasm

926	4	50.0	190	2	T32265	hypothetical prote
927	4	50.0	190	2	C83549	hypothetical prote
928	4	50.0	190	2	B83321	hypothetical prote
929	4	50.0	190	2	G84018	hypothetical prote
930	4	50.0	190	2	E91200	type III secretion
931	4	50.0	190	2	A86047	escJ [imported] -
932	4	50.0	190	2	AG2487	hypothetical prote
933	4	50.0	191	2	S62409	40s ribosomal prot
934	4	50.0	191	2	A57254	thioredoxin-like p
935	4	50.0	191	2	AG0666	probable exported
936	4	50.0	191	2	A72202	hypothetical prote
937	4	50.0	191	2	T31594	hypothetical prote
938	4	50.0	191	2	H83151	hypothetical prote
939	4	50.0	192	2	S22981	T-cell surface gly
940	4	50.0	192	2	JC4663	T-cell receptor CD
941	4	50.0	192	2	T40083	40s ribosomal prot
942	4	50.0	192	2	S60873	phosphorylation-ac
943	4	50.0	192	2	G84287	flavoprotein [impo
944	4	50.0	192	2	T13225	hypothetical prote
945	4	50.0	192	2	F72338	conserved hypothet
946	4	50.0	192	2	A75568	hypothetical prote
947	4	50.0	192	2	A98019	hypothetical prote
948	4	50.0	193	1	H69398	probable phosphoes
949	4	50.0	193	2	D71731	ribonuclease H II
950	4	50.0	193	2	E87346	hypothetical prote
951	4	50.0	193	2	A49704	transcription init
952	4	50.0	193	2	D83620	hypothetical prote
953	4	50.0	194	2	G82623	holliday junction
954	4	50.0	194	2	A83818	heat-shock protein
955	4	50.0	194	2	S72164	2-hydroxychromene-
956	4	50.0	194	2	G81726	conserved hypothet
957	4	50.0	194	2	A99456	hypothetical prote
958	4	50.0	194	2	AG2861	transcription regu
959	4	50.0	194	2	F97638	hypothetical prote
960	4	50.0	195	2	A53746	interferon, tropho
961	4	50.0	195	2	S31287	ribosomal protein
962	4	50.0	195	2	G75635	hypothetical prote
963	4	50.0	195	2	B70577	hypothetical prote
964	4	50.0	195	2	D87256	nitroreductase fam
965	4	50.0	195	2	F75341	transcription regu
966	4	50.0	195	2	D95946	probable guanylate
967	4	50.0	196	2	F75324	phosphoribosylglyc
968	4	50.0	196	2	C69839	3'-phosphoadenosin
969	4	50.0	196	2	B86653	hypothetical prote
970	4	50.0	196	2	S01056	early light-induce
971	4	50.0	196	2	S72861	hypothetical prote
972	4	50.0	196	2	A75402	transcription regu
973	4	50.0	196	2	F71226	hypothetical prote
974	4	50.0	196	2	T35727	probable transcrip
975	4	50.0	197	1	S16822	ribosomal protein
976	4	50.0	197	2	T44358	hypothetical prote
977	4	50.0	197	2	F82921	conserved hypothet
978	4	50.0	197	2	H75563	transcription regu
979	4	50.0	197	2	S53334	streptokinase - St
980	4	50.0	197	2	E71692	NADH2 dehydrogenas
981	4	50.0	198	2	T40123	ubiquitin-conjugat
982	4	50.0	198	2	S14665	probable calcium-b

983	4	50.0	198	2	S55311	TATA-binding prote
984	4	50.0	198	2	AF1887	hypothetical prote
985	4	50.0	198	2	A99647	probable fimbrial-
986	4	50.0	199	2	C71979	urease accessory p
987	4	50.0	199	2	D64528	urease accessory p
988	4	50.0	199	2	C90505	conserved hypothet
989	4	50.0	199	2	H70709	hypothetical prote
990	4	50.0	199	2	E75126	hypothetical prote
991	4	50.0	200	1	TWPO2D	transcription init
992	4	50.0	200	2	S75839	3-isopropylmalate
993	4	50.0	200	2	S10945	transcription init
994	4	50.0	200	2	S10946	transcription init
995	4	50.0	200	2	S61088	transcription init
996	4	50.0	200	2	S21140	transcription init
997	4	50.0	200	2	T21506	hypothetical prote
998	4	50.0	200	2	E96525	protein T1N15.21 [
999	4	50.0	200	2	T05055	hypothetical prote
1000	4	50.0	200	2	AE3268	intracellular sept

ALIGNMENTS

RESULT 1

D42725

nitrile hydratase region 3'-hypothetical protein P47K - *Pseudomonas chlororaphis* (strain B23)

C;Species: *Pseudomonas chlororaphis*

C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 20-Jun-2000

C;Accession: D42725

R;Nishiyama, M.; Horinouchi, S.; Kobayashi, M.; Nagasawa, T.; Yamada, H.; Beppu, T.

J. Bacteriol. 173, 2465-2472, 1991

A;Title: Cloning and characterization of genes responsible for metabolism of nitrile compounds from *Pseudomonas chlororaphis* B23.

A;Reference number: A42725; MUID:91193202; PMID:2013568

A;Accession: D42725

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-419 <NIS>

A;Cross-references: GB:D90216; NID:g216850; PIDN:BAA14247.1; PID:g216854

C;Superfamily: conserved hypothetical protein yciC

Query Match 87.5%; Score 7; DB 2; Length 419;

Best Local Similarity 100.0%; Pred. No. 2;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAE 7

|||||||

Db 48 EVNLDAE 54

RESULT 2

F83867

dihydrodipicolinate synthase BH1742 [imported] - *Bacillus halodurans* (strain C-125)

C;Species: *Bacillus halodurans*

C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: F83867
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji,
F.; Hiramata, C.; Nakamura, Y.; Ogasawara, N.; Kuhara, S.; Horikoshi, K.
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus*
halodurans and genomic sequence comparison with *Bacillus subtilis*.
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: F83867
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-295 <STO>
A;Cross-references: GB:AP001513; GB:BA000004; NID:gl0174345; PIDN:BAB05461.1;
GSPDB:GN00137
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH1742
C;Superfamily: dihydrodipicolinate synthase

Query Match 75.0%; Score 6; DB 2; Length 295;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VNLDAE 7
| | | | |
Db 142 VNLDAE 147

RESULT 3

A83087
conserved hypothetical protein PA4457 [imported] - *Pseudomonas aeruginosa*
(strain PA01)
C;Species: *Pseudomonas aeruginosa*
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: A83087
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey,
M.J.; Brinkman, F.S.L.; Hufnagle, W.O.; Kowalik, D.J.; Lagrou, M.; Garber, R.L.;
Goltry, L.; Tolentino, E.; Westbrook-Wadman, S.; Yuan, Y.; Brody, L.L.; Coulter,
S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, R.M.; Smith, K.A.; Spencer, D.H.;
Wong, G.K.S.; Wu, Z.; Paulsen, I.T.; Reizer, J.; Saier, M.H.; Hancock, R.E.W.;
Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an
opportunistic pathogen.
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: A83087
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-326 <STO>
A;Cross-references: GB:AE004860; GB:AE004091; NID:g9950692; PIDN:AAG07845.1;
GSPDB:GN00131; PASP:PA4457
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA4457
C;Superfamily: probable ATP-binding protein *gutQ*; CBS homology

Query Match 75.0%; Score 6; DB 2; Length 326;

Best Local Similarity 100.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDA 6
|||||
Db 139 EVNLDA 144

RESULT 4

A28825

keratin, type I nonepidermal - African clawed frog

C;Species: *Xenopus laevis* (African clawed frog)

C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 13-Aug-1999

C;Accession: A28825

R;LaFlamme, S.E.; Jamrich, M.; Richter, K.; Sargent, T.D.; Dawid, I.B.

Genes Dev. 2, 853-862, 1988

A;Title: *Xenopus* endo B is a keratin preferentially expressed in the embryonic notochord.

A;Reference number: A28825; MUID:89092007; PMID:2463213

A;Accession: A28825

A;Molecule type: mRNA

A;Residues: 1-368 <LAF>

A;Cross-references: GB:Y00230; NID:g64863; PIDN:CAA68372.1; PID:g64864

C;Genetics:

A;Start codon: GGT

C;Superfamily: cytoskeletal keratin

C;Keywords: coiled coil

Query Match 75.0%; Score 6; DB 2; Length 368;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VNLDAA 7
|||||
Db 220 VNLDAA 225

RESULT 5

F69888

alanine racemase homolog yncD - *Bacillus subtilis*

C;Species: *Bacillus subtilis*

C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000

C;Accession: F69888

R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo,

V.; Bertero, M.G.; Bessieres, P.; Bolotin, A.; Borchert, S.; Boriss, R.;

Boursier, L.; Brans, A.; Braun, M.; Brignell, S.C.; Bron, S.; Brouillet, S.;

Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi, S.K.; Codani,

J.J.; Connerton, I.F.; Cummings, N.J.; Daniel, R.A.; Denizot, F.; Devine, K.M.;

Duesterhoeft, A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.;

Fabret, C.; Ferrari, E.

Nature 390, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi,

A.; Galleron, N.; Ghim, S.Y.; Glaser, P.; Goffeau, A.; Golightly, E.J.; Grandi,

G.; Guiseppi, G.; Guy, B.J.; Haga, K.; Haiech, J.; Harwood, C.R.; Henaut, A.;

Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Itaya, M.; Jones, L.;

Joris, B.; Karamata, D.; Kasahara, Y.; Klaerr-Blanchard, M.; Klein, C.;

Kobayashi, Y.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, S.
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, C.; Medigue, C.; Medina, N.; Mellado, R.P.; Mizuno, M.; Moestl, D.; Nakai, S.; Noback, M.; Noone, D.; O'Reilly, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, D.; Porwolik, S.; Prescott, A.M.; Presecan, E.; Pujic, P.; Purnelle, B.; Rapoport, G.; Rey, M.; Reynolds, S.; Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, E.
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror, S.J.; Serror, P.; Shin, B.S.; Soldo, B.; Sorokin, A.; Tacconi, E.; Takagi, T.; Takahashi, H.; Takemaru, K.; Takeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, S.; Vandenberg, M.; Vannier, F.; Vassarotti, A.; Viari, A.; Wambutt, R.; Wedler, E.; Wedler, H.; Weitzenegger, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: F69888
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-394 <KUN>
A;Cross-references: GB:Z99113; GB:AL009126; NID:g2634090; PIDN:CAB13648.1; PID:g2634148
A;Experimental source: strain 168
C;Genetics:
A;Gene: yncD
C;Superfamily: alanine racemase

Query Match 75.0%; Score 6; DB 2; Length 394;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDA 6
|||||||
Db 11 EVNLDA 16

RESULT 6

JH0776

hydrogenase (EC 1.18.99.1) large chain - *Alcaligenes hydrogenophilus*

C;Species: *Alcaligenes hydrogenophilus*

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C;Accession: JH0776

R;Yagi, K.; Seto, T.; Terakado, M.; Umeda, F.; Doi, T.; Imanishi, T.; Miura, Y.
Chem. Pharm. Bull. 40, 3292-3296, 1992

A;Title: Nucleotide sequences of membrane-bound hydrogenase gene in *Alcaligenes hydrogenophilus*.

A;Reference number: JH0775; MUID:93193199; PMID:1294332

A;Accession: JH0776

A;Molecule type: DNA

A;Residues: 1-619 <YAG>

A;Cross-references: GB:S56898; NID:g299291; PIDN:AAB25780.1; PID:g299293

C;Genetics:

A;Gene: hupL

C;Function:
A;Pathway: hydrogen metabolism
A;Note: contains iron-sulfur and nickel
C;Superfamily: hydrogenase (NiFe) large chain
C;Keywords: hydrogen metabolism; iron; iron-sulfur protein; membrane bound;
metalloprotein; nickel; oxidoreductase
F;75,78,603/Binding site: nickel (Cys) #status predicted
F;78,603/Binding site: iron (Cys) #status predicted
F;82/Active site: His #status predicted

Query Match 75.0%; Score 6; DB 1; Length 619;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVNLDA 6
|||||
Db 33 EVNLDA 38

RESULT 7

C90326

hypothetical protein SSO1653 [imported] - Sulfolobus solfataricus

C;Species: Sulfolobus solfataricus

C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001

C;Accession: C90326

R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-Weiher, C.C.Y.; Clausen, I.G.; Curtis, B.A.; De Moors, A.; Erauso, G.; Fletcher, C.; Gordon, P.M.K.; Heikamp-de Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.; Schenk, M.E.; Theriault, C.; Tolstrup, N.; Charlebois, R.L.; Doolittle, W.F.; Duguet, M.; Gaasterland, T.; Garrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001

A;Description: Sulfolobus solfataricus complete genome.

A;Reference number: A99139

A;Accession: C90326

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-802 <KUR>

A;Cross-references: GB:AE006641; NID:g13814900; PIDN:AAK41866.1; GSPDB:GN00155

C;Genetics:

A;Gene: SSO1653

Query Match 75.0%; Score 6; DB 2; Length 802;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVNLDA 6
|||||
Db 292 EVNLDA 297

RESULT 8

G82193

aminopeptidase N VC1494 [imported] - Vibrio cholerae (strain N16961 serogroup O1)

C;Species: Vibrio cholerae

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001

C;Accession: G82193
 R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.;
 Dodson, R.J.; Haft, D.H.; Hickey, E.K.; Peterson, J.D.; Umayam, L.A.; Gill,
 S.R.; Nelson, K.E.; Read, T.D.; Tettelin, H.; Richardson, D.; Ermolaeva, M.D.;
 Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.; McDonald, L.;
 Utterback, T.; Fleishmann, R.D.; Nierman, W.C.; White, O.; Salzberg, S.L.;
 Smith, H.O.; Colwell, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
 Nature 406, 477-483, 2000
 A;Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio*
cholerae.
 A;Reference number: A82035; MUID:20406833; PMID:10952301
 A;Accession: G82193
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-868 <HEI>
 A;Cross-references: GB:AE004227; GB:AE003852; NID:g9655990; PIDN:AAF94649.1;
 GSPDB:GN00126; TIGR:VC1494
 A;Experimental source: serogroup O1; strain N16961; biotype El Tor
 C;Genetics:
 A;Gene: VC1494
 A;Map position: 1
 C;Superfamily: microsomal aminopeptidase

Query Match 75.0%; Score 6; DB 2; Length 868;
 Best Local Similarity 100.0%; Pred. No. 45;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NLDAEF 8
 |||||
 Db 606 NLDAEF 611

RESULT 9

A54794
 dynein heavy chain, cytosolic - fruit fly (*Drosophila melanogaster*)
 N;Contains: dynein ATPase (EC 3.6.4.2)
 C;Species: *Drosophila melanogaster*
 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 19-Apr-2002
 C;Accession: A54794
 R;Li, M.; McGrail, M.; Serr, M.; Hays, T.S.
 J. Cell Biol. 126, 1475-1494, 1994
 A;Title: *Drosophila* cytoplasmic dynein, a microtubule motor that is
 asymmetrically localized in the oocyte.
 A;Reference number: A54794; MUID:94375524; PMID:8089180
 A;Accession: A54794
 A;Molecule type: mRNA
 A;Residues: 1-4639 <LIA>
 A;Cross-references: GB:L23195; NID:g349668; PIDN:AAA60323.1; PID:g349669
 C;Genetics:
 A;Gene: FlyBase:Dhc64C
 A;Cross-references: FlyBase:FBgn0010349
 C;Superfamily: dynein heavy chain, cytosolic
 C;Keywords: ATP; heterotetramer; hydrolase; microtubule binding; nucleotide
 binding; P-loop
 F;1895-1902/Region: nucleotide-binding motif A (P-loop)
 F;2210-2217/Region: nucleotide-binding motif A (P-loop)
 F;2580-2587/Region: nucleotide-binding motif A (P-loop)

F;2922-2929/Region: nucleotide-binding motif A (P-loop)
F;1901/Binding site: ATP (Lys) #status predicted
F;2216/Binding site: ATP (Lys) #status predicted
F;2586/Binding site: ATP (Lys) #status predicted
F;2928/Binding site: ATP (Lys) #status predicted

Query Match 75.0%; Score 6; DB 1; Length 4639;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 NLDAEF 8
|||||
Db 3885 NLDAEF 3890

RESULT 10

S40015

phd protein - phage P1

C;Species: phage P1

C;Date: 25-Dec-1994 #sequence_revision 23-Feb-1996 #text_change 08-Oct-1999

C;Accession: S40015; S38553

R;Lehnherr, H.; Maguin, E.; Jafri, S.; Yarmolinsky, M.B.

J. Mol. Biol. 233, 414-428, 1993

A;Title: Plasmid addiction genes of bacteriophage P1: doc, which causes cell death on curing of prophage, and phd, which prevents host death when prophage is retained.

A;Reference number: S40015; MUID:94016561; PMID:8411153

A;Accession: S40015

A;Molecule type: DNA

A;Residues: 1-73 <LEH>

A;Cross-references: GB:M95666; NID:g463276; PIDN:AAA16932.1; PID:g215645

R;Schmidt, C.; Lehnherr, H.; Guidolin, A.; Arber, W.

submitted to the EMBL Data Library, November 1992

A;Description: Additional late promoter sequences of bacteriophage P1.

A;Reference number: S38553

A;Accession: S38553

A;Molecule type: DNA

A;Residues: 1-73 <SCH>

A;Cross-references: EMBL:M95666; NID:g463276; PIDN:AAA16932.1; PID:g215645

Query Match 62.5%; Score 5; DB 2; Length 73;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LDAEF 8
|||||
Db 52 LDAEF 56

RESULT 11

S57268

translation elongation factor aEF-1 beta - Sulfolobus solfataricus

C;Species: Sulfolobus solfataricus

C;Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 08-Oct-1999

C;Accession: S57268; S65743

R;Arcari, P.; Raimo, G.; Ianniciello, G.; Gallo, M.; Bocchini, V.

Biochim. Biophys. Acta 1263, 86-88, 1995

A;Title: The first nucleotide sequence of an archaeal elongation factor 1-beta gene.
 A;Reference number: S57268; MUID:95359209; PMID:7632739
 A;Accession: S57268
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-91 <ARC>
 A;Cross-references: EMBL:X76768; NID:g496732; PIDN:CAA54164.1; PID:g496733
 R;Raimo, G.; Masullo, M.; Savino, G.; Scarano, G.; Ianniciello, G.; Parente, A.; Bocchini, V.
 Biochim. Biophys. Acta 1293, 106-112, 1996
 A;Title: Archaeal elongation factor 1-beta is a dimer. Primary structure, molecular and biochemical properties.
 A;Reference number: S65743; MUID:96186282; PMID:8652615
 A;Accession: S65743
 A;Molecule type: protein
 A;Residues: 2-91 <RAI>
 C;Superfamily: Sulfolobus solfataricus translation elongation factor aEF-1 beta
 C;Keywords: homodimer

Query Match 62.5%; Score 5; DB 2; Length 91;
 Best Local Similarity 100.0%; Pred. No. 73;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLD 5
 |||||
 Db 16 EVNLD 20

RESULT 12

A75188
 translation elongation factor ef-1, chain beta PAB3009 - Pyrococcus abyssi (strain Orsay)
 C;Species: Pyrococcus abyssi
 C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
 C;Accession: A75188
 R;anonymous, Genoscope
 submitted to the EMBL Data Library, July 1999
 A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure and evolution.
 A;Reference number: A75001
 A;Accession: A75188
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-91 <KAW>
 A;Cross-references: GB:AJ248283; GB:AL096836; NID:g5457433; PIDN:CAB48952.1; PID:e1514846; PID:g5457461
 A;Experimental source: strain Orsay
 C;Genetics:
 A;Gene: PAB3009

Query Match 62.5%; Score 5; DB 2; Length 91;
 Best Local Similarity 100.0%; Pred. No. 73;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLD 5
 |||||

KW N,N'-Substituted-1,3-diamino-2-hydroxypropane derivative;
KW Alzheimer's disease; Down's syndrome; hereditary cerebral haemorrhage;
KW Dutch-Type amyloidosis; cerebral angiopathy; degenerative dementia;
KW Parkinson's disease; progressive supranuclear palsy;
KW cortical basal degeneration; beta-secretase; amyloid precursor protein;
KW APP; substrate.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Cleavage-site 5. .6

FT /note= "Beta-secretase cleavage site"

XX

PN WO2003040096-A2.

XX

PD 15-MAY-2003.

XX

PF 08-NOV-2002; 2002WO-US036072.

XX

PR 08-NOV-2001; 2001US-0337122P.

PR 28-DEC-2001; 2001US-0344086P.

PR 03-JAN-2002; 2002US-0345635P.

XX

PA (ELAN-) ELAN PHARM INC.

PA (PHAA) PHARMACIA & UPJOHN CO.

XX

PI John V, Maillard M, Jagodzinska B, Beck JP, Gailunas A, Fang L;

PI Sealy J, Tenbrink R, Freskos J, Mickelson J, Samala L, Hom R;

XX

DR WPI; 2003-505059/47.

XX

PT New N,N'-substituted-1,3-diamino-2-hydroxypropane derivatives are beta
PT secretase inhibitors used for treating e.g. Alzheimer's disease, Down's
PT syndrome and hereditary cerebral hemorrhage.

XX

PS Example D; SEQ ID NO 8; 1243pp; English.

XX

CC The invention comprises N,N'-Substituted-1,3-diamino-2-hydroxypropane
CC derivatives. The compounds of the invention are useful for treating:
CC Alzheimer's disease, Down's syndrome, hereditary cerebral haemorrhage
CC with amyloidosis of the Dutch-Type, cerebral angiopathy, degenerative
CC dementia, Parkinson's disease, progressive supranuclear palsy and
CC cortical basal degeneration, and diffuse Lewy body of Alzheimer's
CC disease. The compounds of the invention also inhibit beta-secretase
CC mediated cleavage of amyloid precursor protein (APP). The present amino
CC acid sequence represents a synthetic oligopeptide substrate that can be
CC cleaved by beta-secretase.

XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 8; DB 7; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.4e+06;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVNLDAEF 8

|||||||

Db 2 EVNLDAEF 9

RESULT 36

ADC26557

ID ADC26557 standard; peptide; 9 AA.

XX

AC ADC26557;

XX

DT 18-DEC-2003 (first entry)

XX

DE Beta-secretase cleavage site peptide SEQ ID 4.

XX

KW nootropic; neuroprotective; Alzheimer's disease;

KW beta-secretase cleavage site.

XX

OS Unidentified.

XX

PN WO2003065012-A2.

XX

PD 07-AUG-2003.

XX

PF 03-FEB-2003; 2003WO-US003236.

XX

PR 01-FEB-2002; 2002US-00066319.

XX

PA (UNMI) UNIV MICHIGAN.

XX

PI Ross BD, Rehemtulla A;

XX

DR WPI; 2003-663499/62.

XX

PT New chimeric polypeptides and nucleic acids, useful for detecting and

PT measuring protease activity, for identifying modulators of protease

PT activity for detecting and for preventing or ameliorating Alzheimer's

PT disease.

XX

PS Claim 15; SEQ ID NO 4; 41pp; English.

XX

CC The invention relates to a novel chimeric nucleic acid encoding a
 CC polypeptide which comprises first, second and third domains, where the
 CC first domain comprises a Golgi retention signal peptide or an endoplasmic
 CC reticulum (ER) retention signal peptide, the second domain comprises a
 CC protease cleavage site and the third domain comprises a reporter molecule
 CC and where the protease cleavage site is between the Golgi retention
 CC signal peptide and the reporter molecule. The molecules of the invention
 CC demonstrate nootropic and neuroprotective activities and may be useful
 CC for detecting and measuring protease activity or for identifying
 CC modulators of protease activity in order to detect, prevent or ameliorate
 CC Alzheimer's disease. The current sequence is that of the beta-secretase
 CC cleavage site peptide SEQ ID 4 of the invention.

XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 8; DB 7; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.4e+06;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAEF 8
 |||||||
Db 2 EVNLDAEF 9

RESULT 37

ADC10532

ID ADC10532 standard; peptide; 9 AA.

XX

AC ADC10532;

XX

DT 18-DEC-2003 (first entry)

XX

DE Synthetic beta secretase substrate, SEQ ID NO:8.

XX

KW Substituted hydroxyethylamine; beta secretase inhibitor;

KW amyloid precursor protein; APP; amyloid beta peptide; A beta;

KW neurodegenerative disorder; Alzheimer's disease;

KW mild cognitive impairment; MCI; Down's syndrome;

KW Hereditary Cerebral Haemorrhage with Amyloidosis of the Dutch-type;

KW HCHWAD; cerebral amyloid angiopathy; degenerative dementia;

KW Parkinson's disease; progressive supranuclear palsy;

KW cortical basal degeneration;

KW diffuse Lewy body type of Alzheimer's disease; lobar haemorrhage;

KW nootropic; neuroprotective; cerebroprotective; haemostatic; vasotropic;

KW synthetic substrate.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Cleavage-site 5. .6

FT /note= "Beta secretase cleavage site"

XX

PN WO2003072535-A2.

XX

PD 04-SEP-2003.

XX

PF 27-FEB-2003; 2003WO-US007287.

XX

PR 27-FEB-2002; 2002US-0359953P.

XX

PA (ELAN-) ELAN PHARM INC.

PA (PHAA) PHARMACIA & UPJOHN.

XX

PI Varghese J, Jagodzinska B, Maillard M, Beck JP, Tenbrink RE;

PI Getman D;

XX

DR WPI; 2003-731584/69.

XX

PT New substituted hydroxyethylamines, useful for the treatment of

PT Alzheimer's disease, mild cognitive impairment and dementia, are beta-

PT secretase, beta-amyloid peptide production inhibitor, and beta-deposition

PT inhibitors.

XX

PS Example D; Page 428; 483pp; English.

XX

CC The invention relates to substituted hydroxyethylamines or their salts

CC which are of use in the treatment of Alzheimer's disease and other
 CC neurodegenerative disorders. The compounds act as beta secretase
 CC inhibitors, preventing the cleavage of amyloid precursor protein (APP) to
 CC form the amyloid beta (A beta) peptide. The amyloid beta peptide is
 CC deposited as plaques, which is thought to play a key role in the
 CC pathogenesis of Alzheimer's disease. The compounds of the invention may
 CC be used for the treatment or prevention of Alzheimer's disease, mild
 CC cognitive impairment (MCI), Down's syndrome, Hereditary Cerebral
 CC Haemorrhage with Amyloidosis of the Dutch-type (HCHWAD), cerebral amyloid
 CC angiopathy, other degenerative dementias (including dementias of mixed
 CC vascular and degenerative origin, dementia associated with Parkinson's
 CC disease, dementia associated with progressive supranuclear palsy,
 CC dementia associated with cortical basal degeneration) and diffuse Lewy
 CC body type of Alzheimer's disease. The compounds are also useful in
 CC preventing or delaying the onset of Alzheimer's disease in those who
 CC would progress from mild cognitive impairment to Alzheimer's disease, and
 CC for preventing the potential consequences of cerebral amyloid angiopathy
 CC (i.e., single and recurrent lobar haemorrhages). Sequences ADC10529-
 CC ADC10531 represent synthetic substrates which can be used to assay beta-
 CC secretase activity in the presence or absence of test compounds of the
 CC invention.

XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 8; DB 7; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVNLDAEF 8
 |||||
 Db 2 EVNLDAEF 9

RESULT 38

ADD80769

ID ADD80769 standard; peptide; 9 AA.

XX

AC ADD80769;

XX

DT 29-JAN-2004 (first entry)

XX

DE Synthetic APP-like peptide #6.

XX

KW APP; amyloid precursor protein; Alzheimer's disease; beta-secretase;

KW nootropic; neuroprotective; cerebroprotective; hemostatic;

KW mild cognitive impairment; MCI; Down's syndrome;

KW hereditary cerebral haemorrhage; Dutch-type amyloidosis;

KW cerebral amyloid angiopathy; degenerative dementia; diffuse Lewy body;

KW amyloid beta protein.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Cleavage-site 5. .6

FT /note= "Beta secretase cleavage site"

XX

PN US2003109559-A1.

XX
 PD 12-JUN-2003.
 XX
 PF 11-JUL-2002; 2002US-00193044.
 XX
 PR 11-JUL-2001; 2001US-0304525P.
 PR 30-JUL-2001; 2001US-0308756P.
 PR 17-DEC-2001; 2001US-0341341P.
 PR 17-DEC-2001; 2001US-0341416P.
 PR 21-DEC-2001; 2001US-0344872P.
 PR 14-MAY-2002; 2002US-0380574P.
 XX
 PA (GAIL/) GAILUNAS A.
 PA (TUCK/) TUCKER J A.
 PA (TENB/) TENBRINK R.
 PA (MICK/) MICKELSON J.
 XX
 PI Gailunas A, Tucker JA, Tenbrink R, Mickelson J;
 XX
 DR WPI; 2003-863424/80.
 XX
 PT New N-(3-amino-2-hydroxy-propyl)substituted alkylamide compounds are beta
 PT -secretase activity inhibitors, useful for treating e.g. Alzheimer's
 PT disease, Down's syndrome, mild cognitive impairment, cerebral amyloid
 PT angiopathy.
 XX
 PS Example D; SEQ ID NO 8; 70pp; English.
 XX
 CC The invention relates to N-(3-Amino-2-hydroxy-propyl) substituted
 CC alkylamide compounds (of structure detailed in the specification) or
 CC their salts. Also included is the preparation of the N-(3-Amino-2-hydroxy
 CC -propyl) substituted alkylamide compounds. The compounds are useful in a
 CC medicament for treating, preventing or delaying the onset of Alzheimer's
 CC disease, for treating mild cognitive impairment (MCI), Down's syndrome, a
 CC human having a hereditary cerebral haemorrhage with amyloidosis of the
 CC Dutch-type, cerebral amyloid angiopathy, other degenerative dementias and
 CC diffuse Lewy body type of Alzheimer's disease. The compounds are potent
 CC amyloid beta peptide production inhibitors, hence slow down the
 CC progression of Alzheimer's disease and prevent the disease in the initial
 CC phases. The present sequence is a synthetic peptide containing a beta
 CC secretase cleavage site similar to that of APP (amyloid precursor
 CC protein), used to test the compounds of the invention.
 XX
 SQ Sequence 9 AA;

 Query Match 100.0%; Score 8; DB 7; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 EVNLDAEF 8
 |||||
 Db 2 EVNLDAEF 9

 RESULT 39
 AAW08362
 ID AAW08362 standard; peptide; 10 AA.

XX
 AC AAW08362;
 XX
 DT 05-SEP-1997 (first entry)
 XX
 DE Beta-secretase substrate #3.
 XX
 KW Beta-cleavage site; beta amyloid precursor protein; APP; beta-secretase;
 KW alpha-secretase; proteolytic cleavage; inhibitor; Alzheimer's disease.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1
 FT /note= "acetylated"
 XX
 PN WO9640885-A2.
 XX
 PD 19-DEC-1996.
 XX
 PF 07-JUN-1996; 96WO-US009985.
 XX
 PR 07-JUN-1995; 95US-00480498.
 PR 07-JUN-1995; 95US-00485152.
 XX
 PA (ATHE-) ATHENA NEUROSCIENCES INC.
 XX
 PI Chrysler SMS, Sinha S, Keim PS, Anderson JP, Jacobson-Croak KL;
 PI Tan H, Mcconlogue LC;
 XX
 DR WPI; 1997-052304/05.
 XX
 PT Beta-secretase which specifically cleaves beta-amyloid precursor protein
 PT - useful to screen for inhibitors useful in treatment of Alzheimer's
 PT disease.
 XX
 PS Disclosure; Page 45; 92pp; English.
 XX
 CC AAW08359-W08362 represent substrates for the enzyme of the invention. The
 CC enzyme of the invention is beta-secretase, and specifically cleaves beta-
 CC amyloid precursor protein (beta-APP). Normal processing of beta-APP is
 CC thought to occur via cleavage between residues 16 and 17 of the beta-
 CC amyloid peptide region by an alpha-secretase. Pathogenic processing is
 CC thought to occur by beta-secretase cleavage of beta-APP. Beta-secretase
 CC activity can be detected and measured using a method of the invention,
 CC which detects at least one of the beta-secretase cleavage products formed
 CC on cleavage. The method can be used to determine whether a test substance
 CC inhibits proteolytic cleavage, by beta-secretase, of beta-APP. Compounds
 CC effective to at least partially inhibit beta-secretase activity can be
 CC used to inhibit cleavage of beta-APP in cells or mammalian hosts.
 CC Isolation and purification of beta-secretase will permit chemical
 CC modelling of a critical event in the pathology of Alzheimer's disease
 XX
 SQ Sequence 10 AA;

Query Match 100.0%; Score 8; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.019;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAEF 8
 |||||||
Db 2 EVNLDAEF 9

RESULT 40

AAY33756

ID AAY33756 standard; protein; 10 AA.

XX

AC AAY33756;

XX

DT 09-NOV-1999 (first entry)

XX

DE Synthetic oligopeptide 5-5'SW.

XX

KW Beta-secretase; beta-amyloid protein precursor; APP; Down's syndrome;
KW Alzheimer's disease; measure activity; cleavage site.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "N-terminal Ser is acetylated"

XX

PN US5942400-A.

XX

PD 24-AUG-1999.

XX

PF 07-JUN-1996; 96US-00659984.

XX

PR 07-JUN-1995; 95US-00480498.

PR 07-JUN-1995; 95US-00485152.

XX

PA (ELAN-) ELAN PHARM INC.

XX

PI Sinha S, Jacobson-Croak KL, Anderson JP;

XX

DR WPI; 1999-517417/43.

XX

PT A method for detecting human beta-secretase cleavage of polypeptides
PT useful for identifying beta-secretase inhibitors.

XX

PS Example; Col 30; 43pp; English.

XX

CC Sequences AAY33752-Y33756 are synthetic oligopeptides used for measuring
CC the activity of beta-secretase (AAY33741). Beta-secretase is capable of
CC cleaving beta-amyloid protein precursor (APP) (AAY33742). These synthetic
CC peptides contain the cleavage site of APP. Beta-secretase and APP are
CC used in a method for detecting human beta-secretase cleavage of
CC polypeptides and for identifying beta-secretase inhibitors. Inhibition of
CC beta-secretase activity would be useful for chemical modelling of a
CC critical event in the pathology of Alzheimer's disease. Inhibitors of
CC beta-secretase would be useful for the prevention and treatment of
CC Alzheimer's disease and Down's Syndrome

XX

SQ Sequence 10 AA;

Query Match 100.0%; Score 8; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.019;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAEF 8

|||||||

Db 2 EVNLDAEF 9

Search completed: March 26, 2004, 15:33:30

Job time : 93.5 secs

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OM protein - protein search, using sw model

Run on: March 26, 2004, 15:30:37 ; Search time 16.5 Seconds
(without alignments)
25.031 Million cell updates/sec

Title: US-09-668-314C-71
Perfect score: 8
Sequence: 1 EVNLDAEF 8

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 389414 seqs, 51625971 residues

Word size : 0

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Issued Patents AA:*
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5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length DB	ID	Description
1	8	100.0 9 3	US-08-802-981-219	Sequence 219, App
2	8	100.0 9 4	US-09-724-566A-52	Sequence 52, Appl
3	8	100.0 9 4	US-09-724-566A-83	Sequence 83, Appl
4	8	100.0 10 2	US-08-659-984A-19	Sequence 19, Appl
5	8	100.0 10 3	US-08-660-531-19	Sequence 19, Appl
6	8	100.0 10 4	US-09-548-372D-63	Sequence 63, Appl
7	8	100.0 10 4	US-09-548-367D-63	Sequence 63, Appl
8	8	100.0 10 4	US-09-551-853D-63	Sequence 63, Appl
9	8	100.0 10 4	US-09-604-608-5	Sequence 5, Appli
10	8	100.0 11 5	PCT-US94-07043A-3	Sequence 3, Appli
11	8	100.0 21 2	US-08-659-984A-18	Sequence 18, Appl

12	8	100.0	21	3	US-08-802-981-112	Sequence 112, App
13	8	100.0	21	3	US-08-660-531-18	Sequence 18, Appl
14	8	100.0	30	2	US-08-659-984A-17	Sequence 17, Appl
15	8	100.0	30	3	US-08-660-531-17	Sequence 17, Appl
16	8	100.0	30	4	US-09-724-566A-53	Sequence 53, Appl
17	8	100.0	33	2	US-08-659-984A-16	Sequence 16, Appl
18	8	100.0	33	3	US-08-660-531-16	Sequence 16, Appl
19	8	100.0	33	4	US-09-724-566A-63	Sequence 63, Appl
20	8	100.0	42	2	US-08-659-984A-15	Sequence 15, Appl
21	8	100.0	42	3	US-08-660-531-15	Sequence 15, Appl
22	8	100.0	103	3	US-08-339-708A-12	Sequence 12, Appl
23	8	100.0	506	2	US-08-659-984A-21	Sequence 21, Appl
24	8	100.0	506	3	US-08-660-531-21	Sequence 21, Appl
25	8	100.0	506	4	US-09-054-334-4	Sequence 4, Appli
26	8	100.0	695	4	US-09-548-372D-12	Sequence 12, Appl
27	8	100.0	695	4	US-09-548-367D-12	Sequence 12, Appl
28	8	100.0	695	4	US-09-551-853D-12	Sequence 12, Appl
29	8	100.0	697	4	US-09-548-372D-18	Sequence 18, Appl
30	8	100.0	697	4	US-09-548-367D-18	Sequence 18, Appl
31	8	100.0	697	4	US-09-551-853D-18	Sequence 18, Appl
32	6	75.0	371	4	US-09-252-991A-24809	Sequence 24809, A
33	5	62.5	5	1	US-08-480-498-2	Sequence 2, Appli
34	5	62.5	5	2	US-08-659-984A-14	Sequence 14, Appl
35	5	62.5	5	3	US-08-660-531-14	Sequence 14, Appl
36	5	62.5	5	4	US-09-054-334-2	Sequence 2, Appli
37	5	62.5	5	4	US-09-724-566A-51	Sequence 51, Appl
38	5	62.5	7	1	US-08-136-743B-33	Sequence 33, Appl
39	5	62.5	7	1	US-08-136-743B-35	Sequence 35, Appl
40	5	62.5	7	1	US-08-136-743B-56	Sequence 56, Appl
41	5	62.5	7	3	US-09-040-216-29	Sequence 29, Appl
42	5	62.5	9	3	US-08-802-981-220	Sequence 220, App
43	5	62.5	9	3	US-08-802-981-223	Sequence 223, App
44	5	62.5	9	4	US-09-724-566A-84	Sequence 84, Appl
45	5	62.5	21	3	US-08-802-981-113	Sequence 113, App
46	5	62.5	21	3	US-08-802-981-116	Sequence 116, App
47	5	62.5	27	1	US-08-141-324-12	Sequence 12, Appl
48	5	62.5	27	1	US-08-541-902-12	Sequence 12, Appl
49	5	62.5	41	1	US-08-232-018-5	Sequence 5, Appli
50	5	62.5	41	1	US-08-504-047-5	Sequence 5, Appli
51	5	62.5	41	2	US-09-087-855-5	Sequence 5, Appli
52	5	62.5	67	2	US-08-588-258B-6	Sequence 6, Appli
53	5	62.5	67	3	US-08-460-505-6	Sequence 6, Appli
54	5	62.5	67	5	PCT-US96-08295-6	Sequence 6, Appli
55	5	62.5	68	2	US-08-588-258B-10	Sequence 10, Appl
56	5	62.5	68	3	US-08-460-505-10	Sequence 10, Appl
57	5	62.5	68	5	PCT-US96-08295-10	Sequence 10, Appl
58	5	62.5	73	4	US-09-134-001C-4505	Sequence 4505, Ap
59	5	62.5	81	4	US-09-543-681A-7399	Sequence 7399, Ap
60	5	62.5	117	4	US-09-422-569-10	Sequence 10, Appl
61	5	62.5	120	4	US-08-890-865A-13	Sequence 13, Appl
62	5	62.5	120	4	US-08-890-865A-14	Sequence 14, Appl
63	5	62.5	136	4	US-09-205-258-1081	Sequence 1081, Ap
64	5	62.5	141	4	US-09-621-976-5170	Sequence 5170, Ap
65	5	62.5	151	4	US-09-252-991A-30782	Sequence 30782, A
66	5	62.5	169	4	US-09-328-352-5579	Sequence 5579, Ap
67	5	62.5	197	3	US-08-996-408-2	Sequence 2, Appli
68	5	62.5	197	3	US-09-310-847-2	Sequence 2, Appli

69	5	62.5	197	3	US-09-310-845-2	Sequence 2, Appli
70	5	62.5	197	4	US-09-548-023-2	Sequence 2, Appli
71	5	62.5	205	2	US-08-829-110-6	Sequence 6, Appli
72	5	62.5	205	2	US-08-748-483-5	Sequence 5, Appli
73	5	62.5	217	1	US-08-232-018-2	Sequence 2, Appli
74	5	62.5	217	1	US-08-232-018-3	Sequence 3, Appli
75	5	62.5	217	1	US-08-504-047-2	Sequence 2, Appli
76	5	62.5	217	1	US-08-504-047-3	Sequence 3, Appli
77	5	62.5	217	2	US-08-640-808-2	Sequence 2, Appli
78	5	62.5	217	2	US-09-087-855-2	Sequence 2, Appli
79	5	62.5	217	2	US-09-087-855-3	Sequence 3, Appli
80	5	62.5	220	4	US-09-052-089A-4	Sequence 4, Appli
81	5	62.5	235	3	US-09-244-314-2	Sequence 2, Appli
82	5	62.5	235	4	US-09-498-959-2	Sequence 2, Appli
83	5	62.5	246	4	US-09-540-236-2107	Sequence 2107, Ap
84	5	62.5	254	4	US-09-252-991A-32425	Sequence 32425, A
85	5	62.5	286	3	US-09-120-365-78	Sequence 78, Appl
86	5	62.5	286	3	US-09-515-039-78	Sequence 78, Appl
87	5	62.5	291	2	US-08-838-543-6	Sequence 6, Appli
88	5	62.5	315	4	US-09-584-568C-2	Sequence 2, Appli
89	5	62.5	319	1	US-08-597-236-7	Sequence 7, Appli
90	5	62.5	319	1	US-08-746-682A-7	Sequence 7, Appli
91	5	62.5	334	4	US-09-489-039A-12973	Sequence 12973, A
92	5	62.5	341	3	US-08-725-459B-44	Sequence 44, Appl
93	5	62.5	360	4	US-09-134-001C-4278	Sequence 4278, Ap
94	5	62.5	364	4	US-09-134-000C-5030	Sequence 5030, Ap
95	5	62.5	371	4	US-09-252-991A-32719	Sequence 32719, A
96	5	62.5	380	3	US-09-150-133-9	Sequence 9, Appli
97	5	62.5	380	3	US-09-150-141-9	Sequence 9, Appli
98	5	62.5	380	3	US-09-374-493-9	Sequence 9, Appli
99	5	62.5	380	3	US-09-374-824-9	Sequence 9, Appli
100	5	62.5	380	3	US-09-374-492-9	Sequence 9, Appli
101	5	62.5	380	4	US-09-785-343-9	Sequence 9, Appli
102	5	62.5	392	4	US-09-252-991A-30852	Sequence 30852, A
103	5	62.5	394	4	US-09-134-001C-4834	Sequence 4834, Ap
104	5	62.5	400	4	US-09-543-681A-6245	Sequence 6245, Ap
105	5	62.5	422	4	US-09-489-039A-10905	Sequence 10905, A
106	5	62.5	424	4	US-09-205-258-1079	Sequence 1079, Ap
107	5	62.5	425	4	US-09-328-352-4868	Sequence 4868, Ap
108	5	62.5	426	4	US-09-602-472A-59	Sequence 59, Appl
109	5	62.5	434	3	US-08-725-459B-42	Sequence 42, Appl
110	5	62.5	445	4	US-09-252-991A-22368	Sequence 22368, A
111	5	62.5	452	4	US-09-463-712C-8	Sequence 8, Appli
112	5	62.5	452	4	US-09-865-415-6	Sequence 6, Appli
113	5	62.5	456	4	US-09-252-991A-24273	Sequence 24273, A
114	5	62.5	469	2	US-08-968-751-2	Sequence 2, Appli
115	5	62.5	470	4	US-09-052-089A-2	Sequence 2, Appli
116	5	62.5	501	4	US-09-252-991A-18409	Sequence 18409, A
117	5	62.5	568	4	US-09-690-942-6	Sequence 6, Appli
118	5	62.5	591	4	US-09-711-164-425	Sequence 425, App
119	5	62.5	610	4	US-09-489-039A-12251	Sequence 12251, A
120	5	62.5	642	4	US-09-540-236-2216	Sequence 2216, Ap
121	5	62.5	680	4	US-09-731-166-6	Sequence 6, Appli
122	5	62.5	693	4	US-09-081-385-154	Sequence 154, App
123	5	62.5	710	4	US-09-171-461-16	Sequence 16, Appl
124	5	62.5	739	2	US-08-836-943-2	Sequence 2, Appli
125	5	62.5	744	4	US-09-252-991A-29565	Sequence 29565, A

126	5	62.5	825	4	US-09-540-824-26	Sequence 26, Appl
127	5	62.5	998	2	US-08-415-788-7	Sequence 7, Appli
128	5	62.5	1029	2	US-08-415-788-3	Sequence 3, Appli
129	5	62.5	1132	4	US-09-198-452A-466	Sequence 466, App
130	5	62.5	2756	1	US-08-375-709-11	Sequence 11, Appl
131	5	62.5	2756	1	US-08-752-929-11	Sequence 11, Appl
132	5	62.5	2756	3	US-09-090-793-7	Sequence 7, Appli
133	5	62.5	2756	4	US-09-231-899-7	Sequence 7, Appli
134	5	62.5	3340	4	US-09-252-991A-23568	Sequence 23568, A
135	4	50.0	4	4	US-09-054-334-6	Sequence 6, Appli
136	4	50.0	4	4	US-09-513-783A-92	Sequence 92, Appl
137	4	50.0	4	4	US-09-548-372D-66	Sequence 66, Appl
138	4	50.0	4	4	US-09-548-367D-66	Sequence 66, Appl
139	4	50.0	4	4	US-09-551-853D-66	Sequence 66, Appl
140	4	50.0	4	4	US-09-724-566A-104	Sequence 104, App
141	4	50.0	5	1	US-08-143-697-11	Sequence 11, Appl
142	4	50.0	5	2	US-08-422-333-7	Sequence 7, Appli
143	4	50.0	5	6	5187153-6	Patent No. 5187153
144	4	50.0	5	6	5220013-6	Patent No. 5220013
145	4	50.0	5	6	5223482-6	Patent No. 5223482
146	4	50.0	6	5	PCT-US94-07043A-9	Sequence 9, Appli
147	4	50.0	7	2	US-08-792-553-10	Sequence 10, Appl
148	4	50.0	7	4	US-09-129-192C-44	Sequence 44, Appl
149	4	50.0	7	4	US-09-535-852-1123	Sequence 1123, Ap
150	4	50.0	7	4	US-09-579-012-25	Sequence 25, Appl
151	4	50.0	8	3	US-09-188-579-50	Sequence 50, Appl
152	4	50.0	8	3	US-09-315-444-50	Sequence 50, Appl
153	4	50.0	8	4	US-09-721-362-50	Sequence 50, Appl
154	4	50.0	8	4	US-09-548-372D-67	Sequence 67, Appl
155	4	50.0	8	4	US-09-548-367D-67	Sequence 67, Appl
156	4	50.0	8	4	US-09-752-165-70	Sequence 70, Appl
157	4	50.0	8	4	US-09-551-853D-67	Sequence 67, Appl
158	4	50.0	8	4	US-09-604-608-28	Sequence 28, Appl
159	4	50.0	8	4	US-09-535-852-1128	Sequence 1128, Ap
160	4	50.0	9	3	US-08-802-981-221	Sequence 221, App
161	4	50.0	9	4	US-09-294-987-6	Sequence 6, Appli
162	4	50.0	9	4	US-09-724-566A-82	Sequence 82, Appl
163	4	50.0	9	4	US-09-724-566A-85	Sequence 85, Appl
164	4	50.0	9	4	US-09-724-566A-86	Sequence 86, Appl
165	4	50.0	9	4	US-09-724-566A-88	Sequence 88, Appl
166	4	50.0	9	4	US-09-724-566A-91	Sequence 91, Appl
167	4	50.0	9	4	US-09-535-852-1133	Sequence 1133, Ap
168	4	50.0	10	1	US-07-766-351-1	Sequence 1, Appli
169	4	50.0	10	1	US-08-059-032-1	Sequence 1, Appli
170	4	50.0	10	1	US-08-371-930-12	Sequence 12, Appl
171	4	50.0	10	1	US-08-143-697-10	Sequence 10, Appl
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173	4	50.0	10	4	US-09-548-372D-64	Sequence 64, Appl
174	4	50.0	10	4	US-09-548-367D-64	Sequence 64, Appl
175	4	50.0	10	4	US-09-551-853D-64	Sequence 64, Appl
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187	4	50.0	14	3	US-08-715-106-2	Sequence 2, Appli
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189	4	50.0	14	4	US-09-724-566A-97	Sequence 97, Appl
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193	4	50.0	15	4	US-09-548-372D-71	Sequence 71, Appl
194	4	50.0	15	4	US-09-548-367D-71	Sequence 71, Appl
195	4	50.0	15	4	US-09-551-853D-71	Sequence 71, Appl
196	4	50.0	15	4	US-09-947-372A-48	Sequence 48, Appl
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199	4	50.0	16	2	US-08-986-948-10	Sequence 10, Appl
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204	4	50.0	19	1	US-08-167-919A-3	Sequence 3, Appli
205	4	50.0	19	3	US-08-715-106-3	Sequence 3, Appli
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207	4	50.0	19	4	US-09-442-649-3	Sequence 3, Appli
208	4	50.0	20	1	US-07-678-974D-32	Sequence 32, Appl
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210	4	50.0	20	2	US-08-945-168-37	Sequence 37, Appl
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239	4	50.0	28	3	US-09-388-890-7	Sequence 7, Appli

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277	4	50.0	35	2	US-08-612-785B-40	Sequence 40, Appl
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322	4	50.0	42	1	US-08-304-585-2	Sequence 2, Appli
323	4	50.0	42	1	US-08-302-808-5	Sequence 5, Appli
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446	4	50.0	64	4	US-09-419-281-87	Sequence 87, Appl
447	4	50.0	64	4	US-09-401-415-3	Sequence 3, Appli
448	4	50.0	65	3	US-08-995-156A-43	Sequence 43, Appl
449	4	50.0	65	3	US-08-995-156A-88	Sequence 88, Appl
450	4	50.0	65	4	US-09-419-281-43	Sequence 43, Appl
451	4	50.0	65	4	US-09-419-281-88	Sequence 88, Appl
452	4	50.0	66	3	US-08-995-156A-44	Sequence 44, Appl
453	4	50.0	66	3	US-08-995-156A-89	Sequence 89, Appl
454	4	50.0	66	4	US-09-419-281-44	Sequence 44, Appl
455	4	50.0	66	4	US-09-419-281-89	Sequence 89, Appl
456	4	50.0	66	4	US-09-621-976-4404	Sequence 4404, Ap
457	4	50.0	67	3	US-08-995-156A-45	Sequence 45, Appl
458	4	50.0	67	3	US-08-995-156A-90	Sequence 90, Appl
459	4	50.0	67	4	US-09-419-281-45	Sequence 45, Appl
460	4	50.0	67	4	US-09-419-281-90	Sequence 90, Appl
461	4	50.0	67	4	US-09-621-976-6180	Sequence 6180, Ap
462	4	50.0	67	4	US-09-027-258-1	Sequence 1, Appli
463	4	50.0	68	3	US-08-995-156A-46	Sequence 46, Appl
464	4	50.0	68	3	US-08-995-156A-91	Sequence 91, Appl
465	4	50.0	68	3	US-09-367-953B-35	Sequence 35, Appl
466	4	50.0	68	4	US-09-419-281-46	Sequence 46, Appl
467	4	50.0	68	4	US-09-419-281-91	Sequence 91, Appl

468	4	50.0	68	4	US-09-489-039A-10589	Sequence 10589, A
469	4	50.0	69	1	US-08-056-200-115	Sequence 115, App
470	4	50.0	69	2	US-08-800-644-115	Sequence 115, App
471	4	50.0	69	3	US-08-995-156A-47	Sequence 47, Appl
472	4	50.0	69	3	US-08-995-156A-92	Sequence 92, Appl
473	4	50.0	69	4	US-09-419-281-47	Sequence 47, Appl
474	4	50.0	69	4	US-09-419-281-92	Sequence 92, Appl
475	4	50.0	70	3	US-08-995-156A-48	Sequence 48, Appl
476	4	50.0	70	3	US-08-995-156A-93	Sequence 93, Appl
477	4	50.0	70	4	US-09-419-281-48	Sequence 48, Appl
478	4	50.0	70	4	US-09-419-281-93	Sequence 93, Appl
479	4	50.0	70	4	US-09-620-956-33	Sequence 33, Appl
480	4	50.0	70	4	US-09-611-152-33	Sequence 33, Appl
481	4	50.0	70	4	US-09-631-531-33	Sequence 33, Appl
482	4	50.0	71	3	US-08-995-156A-49	Sequence 49, Appl
483	4	50.0	71	3	US-08-995-156A-94	Sequence 94, Appl
484	4	50.0	71	4	US-09-419-281-49	Sequence 49, Appl
485	4	50.0	71	4	US-09-419-281-94	Sequence 94, Appl
486	4	50.0	71	4	US-09-107-532A-6459	Sequence 6459, Ap
487	4	50.0	72	3	US-08-995-156A-50	Sequence 50, Appl
488	4	50.0	72	3	US-08-995-156A-95	Sequence 95, Appl
489	4	50.0	72	4	US-09-419-281-50	Sequence 50, Appl
490	4	50.0	72	4	US-09-419-281-95	Sequence 95, Appl
491	4	50.0	72	4	US-09-134-001C-3056	Sequence 3056, Ap
492	4	50.0	73	3	US-08-995-156A-51	Sequence 51, Appl
493	4	50.0	73	3	US-08-995-156A-96	Sequence 96, Appl
494	4	50.0	73	4	US-09-419-281-51	Sequence 51, Appl
495	4	50.0	73	4	US-09-419-281-96	Sequence 96, Appl
496	4	50.0	73	4	US-09-134-001C-3436	Sequence 3436, Ap
497	4	50.0	73	4	US-09-622-782-8	Sequence 8, Appli
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499	4	50.0	74	3	US-08-995-156A-97	Sequence 97, Appl
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501	4	50.0	74	4	US-09-419-281-97	Sequence 97, Appl
502	4	50.0	74	4	US-09-585-173B-46	Sequence 46, Appl
503	4	50.0	74	4	US-09-621-976-4325	Sequence 4325, Ap
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505	4	50.0	75	3	US-08-995-156A-98	Sequence 98, Appl
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508	4	50.0	76	3	US-08-995-156A-54	Sequence 54, Appl
509	4	50.0	76	3	US-08-995-156A-99	Sequence 99, Appl
510	4	50.0	76	4	US-09-419-281-54	Sequence 54, Appl
511	4	50.0	76	4	US-09-419-281-99	Sequence 99, Appl
512	4	50.0	76	4	US-09-621-976-5394	Sequence 5394, Ap
513	4	50.0	77	3	US-08-995-156A-55	Sequence 55, Appl
514	4	50.0	77	3	US-08-995-156A-100	Sequence 100, App
515	4	50.0	77	4	US-09-419-281-55	Sequence 55, Appl
516	4	50.0	77	4	US-09-419-281-100	Sequence 100, App
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518	4	50.0	78	3	US-08-995-156A-56	Sequence 56, Appl
519	4	50.0	78	3	US-08-995-156A-101	Sequence 101, App
520	4	50.0	78	4	US-09-419-281-56	Sequence 56, Appl
521	4	50.0	78	4	US-09-419-281-101	Sequence 101, App
522	4	50.0	79	3	US-08-995-156A-57	Sequence 57, Appl
523	4	50.0	79	3	US-08-995-156A-102	Sequence 102, App
524	4	50.0	79	4	US-09-419-281-57	Sequence 57, Appl

525	4	50.0	79	4	US-09-419-281-102	Sequence 102, App
526	4	50.0	79	4	US-09-252-991A-32023	Sequence 32023, A
527	4	50.0	80	3	US-08-995-156A-58	Sequence 58, Appl
528	4	50.0	80	3	US-08-995-156A-103	Sequence 103, App
529	4	50.0	80	4	US-09-419-281-58	Sequence 58, Appl
530	4	50.0	80	4	US-09-419-281-103	Sequence 103, App
531	4	50.0	80	4	US-09-621-976-4091	Sequence 4091, Ap
532	4	50.0	81	3	US-08-995-156A-59	Sequence 59, Appl
533	4	50.0	81	3	US-08-995-156A-104	Sequence 104, App
534	4	50.0	81	4	US-09-419-281-59	Sequence 59, Appl
535	4	50.0	81	4	US-09-419-281-104	Sequence 104, App
536	4	50.0	81	4	US-09-636-215-588	Sequence 588, App
537	4	50.0	81	4	US-09-685-166A-588	Sequence 588, App
538	4	50.0	82	3	US-08-995-156A-60	Sequence 60, Appl
539	4	50.0	82	3	US-08-995-156A-105	Sequence 105, App
540	4	50.0	82	4	US-09-419-281-60	Sequence 60, Appl
541	4	50.0	82	4	US-09-419-281-105	Sequence 105, App
542	4	50.0	82	4	US-09-107-532A-6988	Sequence 6988, Ap
543	4	50.0	83	2	US-08-332-562A-87	Sequence 87, Appl
544	4	50.0	83	3	US-08-995-156A-61	Sequence 61, Appl
545	4	50.0	83	3	US-08-995-156A-106	Sequence 106, App
546	4	50.0	83	3	US-09-138-721-19	Sequence 19, Appl
547	4	50.0	83	4	US-09-419-281-61	Sequence 61, Appl
548	4	50.0	83	4	US-09-419-281-106	Sequence 106, App
549	4	50.0	83	4	US-09-543-681A-4559	Sequence 4559, Ap
550	4	50.0	83	4	US-09-621-976-7617	Sequence 7617, Ap
551	4	50.0	84	3	US-08-995-156A-62	Sequence 62, Appl
552	4	50.0	84	3	US-08-995-156A-107	Sequence 107, App
553	4	50.0	84	4	US-08-858-207A-275	Sequence 275, App
554	4	50.0	84	4	US-09-419-281-62	Sequence 62, Appl
555	4	50.0	84	4	US-09-419-281-107	Sequence 107, App
556	4	50.0	85	1	US-08-428-091-4	Sequence 4, Appli
557	4	50.0	85	3	US-08-995-156A-63	Sequence 63, Appl
558	4	50.0	85	3	US-08-995-156A-108	Sequence 108, App
559	4	50.0	85	4	US-09-162-564-7	Sequence 7, Appli
560	4	50.0	85	4	US-09-419-281-63	Sequence 63, Appl
561	4	50.0	85	4	US-09-419-281-108	Sequence 108, App
562	4	50.0	85	4	US-09-107-532A-3668	Sequence 3668, Ap
563	4	50.0	86	3	US-08-995-156A-64	Sequence 64, Appl
564	4	50.0	86	3	US-08-995-156A-109	Sequence 109, App
565	4	50.0	86	4	US-09-419-281-64	Sequence 64, Appl
566	4	50.0	86	4	US-09-419-281-109	Sequence 109, App
567	4	50.0	87	1	US-08-204-740-13	Sequence 13, Appl
568	4	50.0	87	3	US-08-995-156A-65	Sequence 65, Appl
569	4	50.0	87	3	US-08-995-156A-110	Sequence 110, App
570	4	50.0	87	3	US-09-081-167A-13	Sequence 13, Appl
571	4	50.0	87	3	US-09-081-395-13	Sequence 13, Appl
572	4	50.0	87	3	US-09-416-833-13	Sequence 13, Appl
573	4	50.0	87	4	US-09-419-281-65	Sequence 65, Appl
574	4	50.0	87	4	US-09-419-281-110	Sequence 110, App
575	4	50.0	87	5	PCT-US95-02521-13	Sequence 13, Appl
576	4	50.0	88	3	US-08-995-156A-66	Sequence 66, Appl
577	4	50.0	88	3	US-08-995-156A-111	Sequence 111, App
578	4	50.0	88	4	US-09-419-281-66	Sequence 66, Appl
579	4	50.0	88	4	US-09-419-281-111	Sequence 111, App
580	4	50.0	89	3	US-08-995-156A-67	Sequence 67, Appl
581	4	50.0	89	3	US-08-995-156A-112	Sequence 112, App

582	4	50.0	89	4	US-09-419-281-67	Sequence 67, Appl
583	4	50.0	89	4	US-09-419-281-112	Sequence 112, App
584	4	50.0	89	4	US-09-194-468A-22	Sequence 22, Appl
585	4	50.0	89	4	US-09-194-468A-28	Sequence 28, Appl
586	4	50.0	89	4	US-09-328-352-7376	Sequence 7376, Ap
587	4	50.0	90	3	US-08-995-156A-68	Sequence 68, Appl
588	4	50.0	90	3	US-08-995-156A-113	Sequence 113, App
589	4	50.0	90	4	US-09-068-101-2	Sequence 2, Appli
590	4	50.0	90	4	US-09-419-281-68	Sequence 68, Appl
591	4	50.0	90	4	US-09-419-281-113	Sequence 113, App
592	4	50.0	91	3	US-08-995-156A-114	Sequence 114, App
593	4	50.0	91	3	US-08-794-000-2	Sequence 2, Appli
594	4	50.0	91	4	US-09-068-101-4	Sequence 4, Appli
595	4	50.0	91	4	US-09-419-281-114	Sequence 114, App
596	4	50.0	91	4	US-09-489-039A-14151	Sequence 14151, A
597	4	50.0	92	4	US-09-107-532A-4945	Sequence 4945, Ap
598	4	50.0	92	4	US-09-644-460-27	Sequence 27, Appl
599	4	50.0	93	1	US-08-839-710-3	Sequence 3, Appli
600	4	50.0	93	2	US-09-066-262-3	Sequence 3, Appli
601	4	50.0	93	4	US-09-252-991A-29813	Sequence 29813, A
602	4	50.0	94	3	US-09-298-367B-10	Sequence 10, Appl
603	4	50.0	94	4	US-09-489-039A-8934	Sequence 8934, Ap
604	4	50.0	94	4	US-09-489-039A-14002	Sequence 14002, A
605	4	50.0	94	4	US-09-621-976-6221	Sequence 6221, Ap
606	4	50.0	94	4	US-09-540-236-3170	Sequence 3170, Ap
607	4	50.0	95	4	US-09-328-352-8011	Sequence 8011, Ap
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609	4	50.0	97	4	US-09-620-956-26	Sequence 26, Appl
610	4	50.0	97	4	US-09-252-991A-25885	Sequence 25885, A
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613	4	50.0	97	4	US-09-631-531-26	Sequence 26, Appl
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616	4	50.0	99	2	US-08-422-333-3	Sequence 3, Appli
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621	4	50.0	99	2	US-08-710-749-13	Sequence 13, Appl
622	4	50.0	99	2	US-08-710-749-14	Sequence 14, Appl
623	4	50.0	99	2	US-08-710-749-15	Sequence 15, Appl
624	4	50.0	99	2	US-08-710-749-16	Sequence 16, Appl
625	4	50.0	99	2	US-08-710-749-17	Sequence 17, Appl
626	4	50.0	99	3	US-08-339-708A-4	Sequence 4, Appli
627	4	50.0	99	3	US-08-339-708A-6	Sequence 6, Appli
628	4	50.0	99	3	US-08-339-708A-8	Sequence 8, Appli
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630	4	50.0	99	4	US-09-147-875A-13	Sequence 13, Appl
631	4	50.0	99	4	US-09-147-875A-14	Sequence 14, Appl
632	4	50.0	99	4	US-09-147-875A-15	Sequence 15, Appl
633	4	50.0	99	4	US-09-147-875A-16	Sequence 16, Appl
634	4	50.0	99	4	US-09-147-875A-17	Sequence 17, Appl
635	4	50.0	100	1	US-08-202-389-26	Sequence 26, Appl
636	4	50.0	100	4	US-09-620-956-27	Sequence 27, Appl
637	4	50.0	100	4	US-09-611-152-27	Sequence 27, Appl
638	4	50.0	100	4	US-09-631-531-27	Sequence 27, Appl

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642	4	50.0	100	4	US-09-147-875A-5	Sequence 5, Appli
643	4	50.0	100	4	US-09-147-875A-6	Sequence 6, Appli
644	4	50.0	100	4	US-09-147-875A-7	Sequence 7, Appli
645	4	50.0	100	4	US-09-147-875A-8	Sequence 8, Appli
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647	4	50.0	100	4	US-09-147-875A-12	Sequence 12, Appl
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653	4	50.0	101	2	US-08-710-749-3	Sequence 3, Appli
654	4	50.0	101	2	US-08-710-749-4	Sequence 4, Appli
655	4	50.0	101	2	US-08-710-749-5	Sequence 5, Appli
656	4	50.0	101	2	US-08-710-749-6	Sequence 6, Appli
657	4	50.0	101	2	US-08-710-749-7	Sequence 7, Appli
658	4	50.0	101	4	US-09-147-875A-9	Sequence 9, Appli
659	4	50.0	102	2	US-08-710-749-8	Sequence 8, Appli
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661	4	50.0	103	2	US-08-918-727-1	Sequence 1, Appli
662	4	50.0	103	2	US-08-612-785B-2	Sequence 2, Appli
663	4	50.0	103	2	US-08-475-579A-2	Sequence 2, Appli
664	4	50.0	103	2	US-08-920-162A-2	Sequence 2, Appli
665	4	50.0	103	3	US-08-339-708A-10	Sequence 10, Appl
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667	4	50.0	103	3	US-09-356-931-2	Sequence 2, Appli
668	4	50.0	103	4	US-08-703-675C-2	Sequence 2, Appli
669	4	50.0	103	4	US-08-617-267C-2	Sequence 2, Appli
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671	4	50.0	103	4	US-09-010-147B-2	Sequence 2, Appli
672	4	50.0	103	4	US-09-614-912-152	Sequence 152, App
673	4	50.0	105	2	US-08-729-345-1	Sequence 1, Appli
674	4	50.0	105	4	US-08-858-207A-411	Sequence 411, App
675	4	50.0	105	4	US-09-198-452A-406	Sequence 406, App
676	4	50.0	105	4	US-09-328-352-4147	Sequence 4147, Ap
677	4	50.0	105	4	US-09-489-039A-13486	Sequence 13486, A
678	4	50.0	106	2	US-08-553-541B-5	Sequence 5, Appli
679	4	50.0	106	3	US-09-268-202-5	Sequence 5, Appli
680	4	50.0	106	4	US-09-087-031E-11	Sequence 11, Appl
681	4	50.0	108	1	US-08-204-740-11	Sequence 11, Appl
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683	4	50.0	108	3	US-09-081-395-11	Sequence 11, Appl
684	4	50.0	108	3	US-09-416-833-11	Sequence 11, Appl
685	4	50.0	108	5	PCT-US95-02521-11	Sequence 11, Appl
686	4	50.0	109	3	US-09-053-197A-16	Sequence 16, Appl
687	4	50.0	109	4	US-09-085-761A-16	Sequence 16, Appl
688	4	50.0	111	1	US-08-466-886-36	Sequence 36, Appl
689	4	50.0	111	3	US-08-469-617-36	Sequence 36, Appl
690	4	50.0	111	4	US-09-107-532A-3909	Sequence 3909, Ap
691	4	50.0	111	4	US-09-621-976-4863	Sequence 4863, Ap
692	4	50.0	112	4	US-09-543-681A-5916	Sequence 5916, Ap
693	4	50.0	113	4	US-09-543-681A-5577	Sequence 5577, Ap
694	4	50.0	114	4	US-09-621-976-6093	Sequence 6093, Ap
695	4	50.0	115	4	US-09-134-000C-6190	Sequence 6190, Ap

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697	4	50.0	117	4	US-09-345-236B-26	Sequence 26, Appl
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707	4	50.0	119	1	US-08-487-860-8	Sequence 8, Appli
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713	4	50.0	119	3	US-08-995-156A-2	Sequence 2, Appli
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715	4	50.0	119	3	US-09-044-855A-2	Sequence 2, Appli
716	4	50.0	119	4	US-09-419-281-2	Sequence 2, Appli
717	4	50.0	119	5	PCT-US94-05384-2	Sequence 2, Appli
718	4	50.0	119	5	PCT-US96-10087-2	Sequence 2, Appli
719	4	50.0	121	4	US-09-732-210-321	Sequence 321, App
720	4	50.0	121	4	US-09-732-210-386	Sequence 386, App
721	4	50.0	122	2	US-08-958-201-6	Sequence 6, Appli
722	4	50.0	122	4	US-09-194-468A-21	Sequence 21, Appl
723	4	50.0	122	4	US-09-194-468A-27	Sequence 27, Appl
724	4	50.0	122	4	US-09-489-039A-11486	Sequence 11486, A
725	4	50.0	123	4	US-08-858-207A-320	Sequence 320, App
726	4	50.0	123	4	US-09-252-991A-24837	Sequence 24837, A
727	4	50.0	126	4	US-09-231-788-15	Sequence 15, Appl
728	4	50.0	126	4	US-09-252-991A-16600	Sequence 16600, A
729	4	50.0	126	4	US-09-328-352-7886	Sequence 7886, Ap
730	4	50.0	126	4	US-09-543-681A-5264	Sequence 5264, Ap
731	4	50.0	126	4	US-09-621-976-7011	Sequence 7011, Ap
732	4	50.0	127	4	US-08-811-481-5	Sequence 5, Appli
733	4	50.0	127	4	US-09-328-352-5964	Sequence 5964, Ap
734	4	50.0	127	4	US-09-876-527-5	Sequence 5, Appli
735	4	50.0	128	4	US-09-620-956-42	Sequence 42, Appl
736	4	50.0	128	4	US-09-611-152-42	Sequence 42, Appl
737	4	50.0	128	4	US-09-794-705A-27	Sequence 27, Appl
738	4	50.0	128	4	US-09-631-531-42	Sequence 42, Appl
739	4	50.0	129	4	US-09-134-000C-5429	Sequence 5429, Ap
740	4	50.0	130	4	US-09-231-788-27	Sequence 27, Appl
741	4	50.0	131	3	US-09-188-930-156	Sequence 156, App
742	4	50.0	131	3	US-09-188-930-284	Sequence 284, App
743	4	50.0	131	4	US-09-312-283C-156	Sequence 156, App
744	4	50.0	131	4	US-09-312-283C-284	Sequence 284, App
745	4	50.0	131	4	US-09-107-532A-4265	Sequence 4265, Ap
746	4	50.0	131	4	US-09-107-532A-6367	Sequence 6367, Ap
747	4	50.0	131	4	US-09-134-000C-4902	Sequence 4902, Ap
748	4	50.0	132	1	US-08-591-498-16	Sequence 16, Appl
749	4	50.0	132	4	US-09-107-532A-6072	Sequence 6072, Ap
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751	4	50.0	133	1	US-08-268-348A-10	Sequence 10, Appl
752	4	50.0	133	3	US-08-961-083-188	Sequence 188, App

753	4	50.0	133	4	US-09-570-921-54	Sequence 54, Appl
754	4	50.0	133	4	US-09-536-784-188	Sequence 188, App
755	4	50.0	134	4	US-09-570-921-52	Sequence 52, Appl
756	4	50.0	134	4	US-09-570-921-53	Sequence 53, Appl
757	4	50.0	135	3	US-09-293-395-9	Sequence 9, Appli
758	4	50.0	135	3	US-09-668-648-9	Sequence 9, Appli
759	4	50.0	135	4	US-09-489-039A-14134	Sequence 14134, A
760	4	50.0	136	3	US-09-053-197A-37	Sequence 37, Appl
761	4	50.0	136	4	US-09-085-761A-37	Sequence 37, Appl
762	4	50.0	136	4	US-09-489-039A-8896	Sequence 8896, Ap
763	4	50.0	136	4	US-09-621-976-4705	Sequence 4705, Ap
764	4	50.0	139	4	US-09-328-352-7327	Sequence 7327, Ap
765	4	50.0	140	4	US-09-252-991A-26603	Sequence 26603, A
766	4	50.0	141	4	US-09-286-981B-2	Sequence 2, Appli
767	4	50.0	141	4	US-09-543-681A-4953	Sequence 4953, Ap
768	4	50.0	141	4	US-09-540-236-3018	Sequence 3018, Ap
769	4	50.0	142	4	US-09-252-991A-19633	Sequence 19633, A
770	4	50.0	143	1	US-07-710-361-9	Sequence 9, Appli
771	4	50.0	143	4	US-09-134-000C-4294	Sequence 4294, Ap
772	4	50.0	144	1	US-07-956-700B-79	Sequence 79, Appl
773	4	50.0	144	1	US-08-476-537-79	Sequence 79, Appl
774	4	50.0	144	1	US-08-485-607-79	Sequence 79, Appl
775	4	50.0	144	2	US-08-475-879-79	Sequence 79, Appl
776	4	50.0	144	4	US-08-936-165A-445	Sequence 445, App
777	4	50.0	144	4	US-09-433-043B-79	Sequence 79, Appl
778	4	50.0	144	4	US-09-370-838-73	Sequence 73, Appl
779	4	50.0	144	4	US-09-621-976-5120	Sequence 5120, Ap
780	4	50.0	144	4	US-09-621-976-7647	Sequence 7647, Ap
781	4	50.0	145	4	US-09-252-991A-32418	Sequence 32418, A
782	4	50.0	145	4	US-09-621-976-4902	Sequence 4902, Ap
783	4	50.0	146	4	US-08-858-207A-323	Sequence 323, App
784	4	50.0	146	4	US-08-858-207A-494	Sequence 494, App
785	4	50.0	146	4	US-09-228-986-123	Sequence 123, App
786	4	50.0	146	4	US-09-732-210-610	Sequence 610, App
787	4	50.0	146	4	US-09-732-210-623	Sequence 623, App
788	4	50.0	146	4	US-09-732-210-840	Sequence 840, App
789	4	50.0	146	4	US-09-107-532A-6388	Sequence 6388, Ap
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791	4	50.0	147	4	US-09-732-210-845	Sequence 845, App
792	4	50.0	147	4	US-09-732-210-846	Sequence 846, App
793	4	50.0	147	4	US-09-732-210-849	Sequence 849, App
794	4	50.0	147	4	US-09-489-039A-13311	Sequence 13311, A
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796	4	50.0	148	4	US-09-732-210-850	Sequence 850, App
797	4	50.0	149	1	US-08-530-010-15	Sequence 15, Appl
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799	4	50.0	149	3	US-08-714-524D-15	Sequence 15, Appl
800	4	50.0	149	4	US-09-134-001C-4639	Sequence 4639, Ap
801	4	50.0	149	4	US-09-634-238-265	Sequence 265, App
802	4	50.0	149	4	US-09-540-236-2601	Sequence 2601, Ap
803	4	50.0	150	4	US-09-134-001C-3280	Sequence 3280, Ap
804	4	50.0	150	4	US-09-732-210-618	Sequence 618, App
805	4	50.0	151	4	US-09-620-956-38	Sequence 38, Appl
806	4	50.0	151	4	US-09-611-152-38	Sequence 38, Appl
807	4	50.0	151	4	US-09-794-705A-23	Sequence 23, Appl
808	4	50.0	151	4	US-09-732-210-624	Sequence 624, App
809	4	50.0	151	4	US-09-134-000C-5804	Sequence 5804, Ap

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811	4	50.0	152	4	US-09-598-401C-64	Sequence 64, Appl
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813	4	50.0	153	4	US-08-936-165A-507	Sequence 507, App
814	4	50.0	153	4	US-09-620-956-41	Sequence 41, Appl
815	4	50.0	153	4	US-09-611-152-41	Sequence 41, Appl
816	4	50.0	153	4	US-09-794-705A-26	Sequence 26, Appl
817	4	50.0	153	4	US-09-631-531-41	Sequence 41, Appl
818	4	50.0	154	3	US-09-404-670-4	Sequence 4, Appli
819	4	50.0	154	4	US-09-620-956-37	Sequence 37, Appl
820	4	50.0	154	4	US-09-611-152-37	Sequence 37, Appl
821	4	50.0	154	4	US-09-328-352-6330	Sequence 6330, Ap
822	4	50.0	154	4	US-09-794-705A-22	Sequence 22, Appl
823	4	50.0	154	4	US-09-631-531-37	Sequence 37, Appl
824	4	50.0	155	4	US-09-489-039A-13472	Sequence 13472, A
825	4	50.0	156	2	US-08-500-860A-36	Sequence 36, Appl
826	4	50.0	156	4	US-09-543-681A-5954	Sequence 5954, Ap
827	4	50.0	157	4	US-09-620-956-43	Sequence 43, Appl
828	4	50.0	157	4	US-09-611-152-43	Sequence 43, Appl
829	4	50.0	157	4	US-09-794-705A-28	Sequence 28, Appl
830	4	50.0	157	4	US-09-489-039A-9071	Sequence 9071, Ap
831	4	50.0	157	4	US-09-631-531-43	Sequence 43, Appl
832	4	50.0	157	5	PCT-US93-02475-8	Sequence 8, Appli
833	4	50.0	157	5	PCT-US93-02475-9	Sequence 9, Appli
834	4	50.0	158	3	US-09-010-809-18	Sequence 18, Appl
835	4	50.0	158	4	US-09-325-932A-86	Sequence 86, Appl
836	4	50.0	158	4	US-09-724-623-85	Sequence 85, Appl
837	4	50.0	158	4	US-09-620-956-36	Sequence 36, Appl
838	4	50.0	158	4	US-09-620-956-40	Sequence 40, Appl
839	4	50.0	158	4	US-09-611-152-36	Sequence 36, Appl
840	4	50.0	158	4	US-09-611-152-40	Sequence 40, Appl
841	4	50.0	158	4	US-09-328-352-4489	Sequence 4489, Ap
842	4	50.0	158	4	US-09-794-705A-21	Sequence 21, Appl
843	4	50.0	158	4	US-09-794-705A-25	Sequence 25, Appl
844	4	50.0	158	4	US-09-631-531-36	Sequence 36, Appl
845	4	50.0	158	4	US-09-631-531-40	Sequence 40, Appl
846	4	50.0	159	3	US-09-010-809-1	Sequence 1, Appli
847	4	50.0	159	4	US-09-543-681A-8070	Sequence 8070, Ap
848	4	50.0	159	4	US-09-134-000C-5859	Sequence 5859, Ap
849	4	50.0	160	4	US-09-620-956-14	Sequence 14, Appl
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851	4	50.0	160	4	US-09-620-956-16	Sequence 16, Appl
852	4	50.0	160	4	US-09-620-956-17	Sequence 17, Appl
853	4	50.0	160	4	US-09-620-956-18	Sequence 18, Appl
854	4	50.0	160	4	US-09-620-956-19	Sequence 19, Appl
855	4	50.0	160	4	US-09-620-956-20	Sequence 20, Appl
856	4	50.0	160	4	US-09-620-956-21	Sequence 21, Appl
857	4	50.0	160	4	US-09-620-956-22	Sequence 22, Appl
858	4	50.0	160	4	US-09-620-956-23	Sequence 23, Appl
859	4	50.0	160	4	US-09-620-956-24	Sequence 24, Appl
860	4	50.0	160	4	US-09-620-956-25	Sequence 25, Appl
861	4	50.0	160	4	US-09-620-956-39	Sequence 39, Appl
862	4	50.0	160	4	US-09-611-152-14	Sequence 14, Appl
863	4	50.0	160	4	US-09-611-152-15	Sequence 15, Appl
864	4	50.0	160	4	US-09-611-152-16	Sequence 16, Appl
865	4	50.0	160	4	US-09-611-152-17	Sequence 17, Appl
866	4	50.0	160	4	US-09-611-152-18	Sequence 18, Appl

867	4	50.0	160	4	US-09-611-152-19	Sequence 19, Appl
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871	4	50.0	160	4	US-09-611-152-23	Sequence 23, Appl
872	4	50.0	160	4	US-09-611-152-24	Sequence 24, Appl
873	4	50.0	160	4	US-09-611-152-25	Sequence 25, Appl
874	4	50.0	160	4	US-09-611-152-39	Sequence 39, Appl
875	4	50.0	160	4	US-09-794-705A-9	Sequence 9, Appli
876	4	50.0	160	4	US-09-794-705A-10	Sequence 10, Appl
877	4	50.0	160	4	US-09-794-705A-11	Sequence 11, Appl
878	4	50.0	160	4	US-09-794-705A-12	Sequence 12, Appl
879	4	50.0	160	4	US-09-794-705A-13	Sequence 13, Appl
880	4	50.0	160	4	US-09-794-705A-14	Sequence 14, Appl
881	4	50.0	160	4	US-09-794-705A-15	Sequence 15, Appl
882	4	50.0	160	4	US-09-794-705A-16	Sequence 16, Appl
883	4	50.0	160	4	US-09-794-705A-17	Sequence 17, Appl
884	4	50.0	160	4	US-09-794-705A-18	Sequence 18, Appl
885	4	50.0	160	4	US-09-794-705A-19	Sequence 19, Appl
886	4	50.0	160	4	US-09-794-705A-20	Sequence 20, Appl
887	4	50.0	160	4	US-09-794-705A-24	Sequence 24, Appl
888	4	50.0	160	4	US-09-543-681A-7071	Sequence 7071, Ap
889	4	50.0	160	4	US-09-489-039A-12737	Sequence 12737, A
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892	4	50.0	160	4	US-09-631-531-16	Sequence 16, Appl
893	4	50.0	160	4	US-09-631-531-17	Sequence 17, Appl
894	4	50.0	160	4	US-09-631-531-18	Sequence 18, Appl
895	4	50.0	160	4	US-09-631-531-19	Sequence 19, Appl
896	4	50.0	160	4	US-09-631-531-20	Sequence 20, Appl
897	4	50.0	160	4	US-09-631-531-21	Sequence 21, Appl
898	4	50.0	160	4	US-09-631-531-22	Sequence 22, Appl
899	4	50.0	160	4	US-09-631-531-23	Sequence 23, Appl
900	4	50.0	160	4	US-09-631-531-24	Sequence 24, Appl
901	4	50.0	160	4	US-09-631-531-25	Sequence 25, Appl
902	4	50.0	160	4	US-09-631-531-39	Sequence 39, Appl
903	4	50.0	161	4	US-09-252-991A-25087	Sequence 25087, A
904	4	50.0	161	4	US-09-252-991A-29145	Sequence 29145, A
905	4	50.0	161	4	US-09-328-352-6732	Sequence 6732, Ap
906	4	50.0	161	4	US-09-328-352-7968	Sequence 7968, Ap
907	4	50.0	162	2	US-08-716-317-10	Sequence 10, Appl
908	4	50.0	162	4	US-09-134-000C-4598	Sequence 4598, Ap
909	4	50.0	162	6	5220013-4	Patent No. 5220013
910	4	50.0	162	6	5223482-4	Patent No. 5223482
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912	4	50.0	163	4	US-09-489-039A-12971	Sequence 12971, A
913	4	50.0	164	1	US-08-318-193-60	Sequence 60, Appl
914	4	50.0	164	3	US-08-860-339-24	Sequence 24, Appl
915	4	50.0	164	3	US-09-148-680-4	Sequence 4, Appli
916	4	50.0	164	4	US-09-134-000C-3529	Sequence 3529, Ap
917	4	50.0	164	4	US-09-573-629-24	Sequence 24, Appl
918	4	50.0	165	4	US-09-252-991A-31106	Sequence 31106, A
919	4	50.0	165	4	US-09-489-039A-9399	Sequence 9399, Ap
920	4	50.0	165	4	US-09-134-000C-3704	Sequence 3704, Ap
921	4	50.0	165	4	US-09-134-000C-5015	Sequence 5015, Ap
922	4	50.0	166	3	US-08-845-258-43	Sequence 43, Appl
923	4	50.0	166	3	US-08-990-571-43	Sequence 43, Appl